

CC DA expressed by melanoma cells of the subject. Also disclosed are pING
CC vectors containing a sequence encoding the human or mouse tyrosinase
CC genes. The methods and xenogeneic DA are useful for treating canine
CC malignant melanoma (gene therapy) in dog suffering from the disease by
CC administering an immunological amount of the xenogeneic DA and for other
CC mammals. The sequence presented is the vector, heyr-pING, containing the
CC human tyrosinase gene

XX Sequence 6408 BP; 1621 A; 1583 C; 1509 G; 1695 T; 0 U; 0 Other;

Query Match 100.0%; Score 6408; DB 7; Length 6408;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 6408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4081 AGACTTAGGACACAGCAATGCCCAACACCAAGTGTGCGGCAAGAGGCCGTGGCGGTA 4140
DB 4081 AGACTTAGGACACAGCAATGCCCAACACCAAGTGTGCGGCAAGAGGCCGTGGCGGTA 4140
QY 4141 GGGTATGTCTGAAAAATGAGCTCGAGATTGGGCTCGCACCGCTGACGAGATGAAGA 4200
DB 4141 GGGTATGTCTGAAAAATGAGCTCGAGATTGGGCTCGCACCGCTGACGAGATGAAGA 4200
QY 4201 CTTAAGGACAGCGAGAGAAAGATGCAAGGAGCTGATGTTGATTTCTGAAGAGATCA 4260
DB 4201 CTTAAGGACAGCGAGAGAAAGATGCAAGGAGCTGATGTTGATTTCTGAAGAGATCA 4260
QY 4261 GAGGTATCTCCGTTGGGCTGCTTTAAGGTGAAGGAGCTGATGATGAGAGATCA 4320
DB 4261 GAGGTATCTCCGTTGGGCTGCTTTAAGGTGAAGGAGCTGATGATGAGAGATCA 4320
QY 4321 GTTGTCCCGGCGCGGACACAGCATATATAGCTGACAGACTAAACAGCTGTTCTTTC 4380
DB 4321 GTTGTCCCGGCGCGGACACAGCATATATAGCTGACAGACTAAACAGCTGTTCTTTC 4380
QY 4381 ATGGGCTTTTCTGACAGTCAACGCTCAAGCTTATATAGACTCACTATAGGAGACCCAA 4440
DB 4381 ATGGGCTTTTCTGACAGTCAACGCTCAAGCTTATATAGACTCACTATAGGAGACCCAA 4440
QY 4441 GCTGGCTAGCGTTTAACTTAAGCTTGGTACCGAGCTCGATTCACACTAGTCAAGTGGT 4500
DB 4441 GCTGGCTAGCGTTTAACTTAAGCTTGGTACCGAGCTCGATTCACACTAGTCAAGTGGT 4500

QY 4501 GGAATTCGCGGA-----AGAA 4516
DB 4501 GGAATTCGGAACACTATTAACCTATGCTGAGATTTTGTATGATCTAAAGAGAAAA 4560
QY 4517 TGCTCTGGCTGTTTGTATGCTGCTGCTGAGATTTCCAGACCTCGCTGGCATTTTC 4576
DB 4561 TGTCTGGCTGTTTGTATGCTGCTGCTGAGATTTCCAGATCTGATGAGCATTTTC 4620
QY 4577 CTAGAGCTGTGTCTCTTAAGAACCTGATGAGAAAGATGCTCCACCGTGAAGC 4636
DB 4621 CTGAGCTGTGTCTCTCTTAAGAACCTGATGAGAAAGATGCTCCACATGATGAG 4680
QY 4637 GGGACAGAGGTCCCTGGCGCAGCTTCAAGGAGAGGTTCTGTCAGATATCTCTGT 4696
DB 4681 GGTATGAGAGTCCCTGGCGCAGCTTCAAGGAGAGGTTCTGTCAGATATCTCTGT 4740
QY 4697 CCAATGACACCTTGGGCTCAATTTCCCTTCAAGGAGTGAAGCCGAGTCTGGC 4756
DB 4741 CCAATGACACCTTGGAGCTCAATTTCCCTTCAAGGAGTGAAGCCGAGTCTGGC 4800
QY 4757 CTTCGCTTTTATATAGGACCTGCGAGTCTCTGGCACTTCAATGAGTCACTGTG 4816
DB 4801 CCTCTGTGTTTATATAGGACCTGCGAGTCTCAAGGACCTTCAATGAGTCACTGTG 4860
QY 4817 GAAACGCAAGTTGGCTTTGGGACCAACGCAAGAGAGACGACTCTGTGGTGA 4876
DB 4861 GAAACGTAAGTTGGATTTGGGGGCCCAATTTGTAAGAGAGAGGAGTCTTATAGAA 4920
QY 4877 GAAACATCTTGCATTTGAGTGGCCCAAGAGAGCAAAATTTTGGCTTACCTCACTTAC 4936
DB 4921 GAAACATTTTGTATGAGTGTCTCCGAAAGAAATGATTTCTTTCTTACTCACTTAC 4980
QY 4937 CAAAGCATACATCACTGACATATGTCATCCCATAGGAGCTATGCGCAATAGAAA 4996
DB 4981 CAAACATATATCACTGACATATGTCATCCCATAGGAGCTATGCGCAATAGAAA 5040
QY 4997 ATGATCAACACCATGTTTAAAGACATCAATTTTATGACTTGTGCTGATGATGAT 5056
DB 5041 ATGATCAACACCATGTTTAAAGACATCAATTTTATGACTTGTGATGATGATGAT 5100
QY 5057 ATATATGTCAATGAGTCACTGCTGGGAGATATGAAATCTGGAAGACATTTTGG 5116
DB 5101 ATATATGTCAATGAGTCACTGCTGGGAGATATGAAATCTGGAAGACATTTTGG 5160
QY 5117 CCATGAGACACGCTTTTCTGCTGGATGACTTCTTGTGCGGTGGAACAAG 5176
DB 5161 CCATGAGACACGAGGTTTCTGCTGGGACAGACTTCTTGTATGTTGGGAACAAG 5220
QY 5177 AATTCAGAGCTGACAGAGATGAAATCTCATATTTGGAATGGAATGCGGAGATG 5236
DB 5221 AATTCAGAGCTGACAGAGATGAAATCTCATATTTGGAATGGAATGGAATG 5280
QY 5237 CAGAAAGTGTGACATTTGACAGATGATGATCAATGGAAGGTGAGCAACCCCAAAATCTTA 5296
DB 5281 CAGAAAGTGTGACATTTGACAGATGATGATCAATTTGGAAGGTGAGCAACCCCAAAATCTTA 5340
QY 5297 ACTTACTGACCCGAGATCAATTTCTCTCTTGGAGATTTGCTGAGCGATGAGG 5356
DB 5341 ACTTACTGACCCGAGATCTTCTCTCTCTGAGAGATTTGAGAGATGAGAG 5400
QY 5357 AGTACACAGCCATCACTTTATGCAATGGAACGCCGAGGAGACTTTACGGCTATATC 5416
DB 5401 AGTATATATACCTCACTGTTTATGAGATGGAACACTGAGGAGCACTATTAAGTATC 5460
QY 5417 CTGGAACCATGACCAATCTGAGAACCAAGGCTCCCTTCTGAGCTGATGATTTT 5476
DB 5461 CTGGAACCATGACCAACCAAGGAGCAAGGCTCCCTTCTGAGCTGATGATTTT 5520
QY 5477 GCTGAGTTTGAACCAATATGATGATGTTTCAATGATTAAGTGCATTTCACTTTA 5536
DB 5521 GCTGAGTTTGAACCAATATGATGATGATGATGATGATGATGATGATGATGATGAT 5580
QY 5537 GAAATACACTGGAAGATTTGCTATGCTCACTTACTGGAGATGAGGATGCTCTCAAGCA 5596

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5581 GAAACACACTGGAGAGATTTGGCAGTCCACTCAAGGATAGAGATCTTCTCAAGTA 5640
5597 GCATGACAAATGCTTGCACATCATATATGAATGAACAAATGTCAGGATATCG 5656
5641 GCATGACAAATGCTTGCACATCATATATGAATGAACAAATGTCAGGATATCG 5700
5657 CCAAGATCTTATCTTCTTCTTCAACCATGATTTGTGAAGATTTTGAAGATGCG 5716
5701 CCAAGATCTTATTTCTTCTTCTTCAACCATGATTTGTGAAGATTTTGAAGATGCG 5760
5717 TCGAAGGACCGCTCTTCTTCAAGAAATTTATCCAGAACCATGACCATTTGACATA 5776
5761 TCGAAGGACCGCGCTCTTCTTGTGAAGTTTACCAGAACCAATGACCATGCGCCATA 5820
5777 ACCGGAATCTCTATGATGTTCTTTTATACCACTGTACAGAAATGATTTCTTATTT 5836
5821 ACAGAACTCTTACATGTTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 5880
5837 CATCCAAAGATCTGGGCTATGACTATGACTATGACTATGACTATGACTATGACTATG 5896
5881 CATCCAAAGATCTGGGCTATGACTATGACTATGACTATGACTATGACTATGACTATG 5940
5897 AAGACTACATTAAGTCTATTTTGAACAAAGCGAGTCTGCTATGCTATGCTATGCT 5956
5941 GAAATATATTTGAGCCCTTACTTGTGAACAAAGCGAGTCTGCTATGCTATGCTATG 6000
5957 CGGCGATGATGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6016
6001 CAGACTGCTGAGGAGCTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6060
6017 GTC-----ACAAAGAAAGCAAGCTTCTGAAAGAAAGCAAGCTTCTGATGAGA 6067
6061 TTCAGAAAGAAAGAAAGAAAGCAAGCTTCTGAAAGAAAGCAAGCTTCTGATGAGA 6120
6068 AAGAGATTTACCAAGCT---TGTATCAGAGCCATTTATTAAGGCTTAGGCAATAGAT 6124
6121 AAGACGACTACCAAGCTTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6180
6125 AGGCGCAAAAAGCTGACCTCATCTTACT 6154
6181 GGGACTGAAAAGTTTAACTCACTCGACT 6210

RESULT 3
ADD55598/c
ID ADD55598 standard; DNA; 5386 BP.
XX
AC ADD55598;
XX
DT 15-JAN-2004 (first entry)
XX
DE Bistronic eukaryotic expression vector PL190.
XX
KW Multicistronic eukaryotic expression vector; multiple protein expression;
KW simultaneous expression; viral internal ribosomal entry site; viral IRES;
KW chain terminator; transcription pause site; gene transfer;
KW DNA immunisation; gene therapy; PL190; kanamycin resistance gene;
KW cytomegalovirus; CMV promoter/enhancer; CMV intron A;
KW encephalomyocarditis virus; EMCV IRES; SV40 polyadenylation site; cyclic;
KW circular; ds.
XX
XX Chimeric.
OS Synthetic.
OS Human herpesvirus 5.
OS Encephalomyocarditis virus.
OS Simian virus 40.
OS Escherichia coli.
XX
PN MO2003031630-A1.
XX
PD 17-APR-2003.
XX
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PF 10-OCT-2002; 2002MO-IT000646.
XX
PR 12-OCT-2001; 2001IT-MI002110.
XX
PA (KERY-) KERYOS SPA.
XX
PI Fazio V, Rinaldi M, Sonzogni L, Tonon G, Oresini G;
XX WPI; 2003-393446/37.
XX
PT New multicistronic recombinant plasmid vectors expressing two to our
PT genes simultaneously, useful in various biotechnological applications,
PT such as gene transfer, gene therapy and in DNA immunization.
XX
PS Claim 18; SEQ ID NO 1; 52bp; English.
XX
CC The invention relates to multicistronic eukaryotic expression vectors for
CC the expression of at least two proteins of interest which may be
CC identical or different. The vectors comprise at least one eukaryotic
CC expression cassette having a promoter/enhancer sequence, an intron
CC sequence, a cloning site, a viral internal ribosomal entry site (IRES)
CC and a chain terminator. The vectors may additionally contain a
CC transcription pause site downstream of the chain terminator. The
CC invention also encompasses eukaryotic host cells comprising a vector of
CC the invention, and the recombinant expression of two or more eukaryotic
CC proteins using host cells transformed with a vector of the invention.
CC The vectors are useful in various biotechnological applications in which
CC the simultaneous expression of two or more genes is necessary, such as
CC gene transfer protocols, DNA immunisation, or for the expression of
CC different molecules in the same cell. They may also be used in gene
CC therapy. The present sequence represents a specifically claimed vector
CC designated PL190, which comprises a cytomegalovirus (CMV)
CC promoter/enhancer, CMV intron A, the encephalomyocarditis virus (EMCV)
CC IRES, an SV40 polyadenylation site and a transcription pause site, as
CC well as a kanamycin resistance gene.
XX
SQ Sequence 5386 BP; 1353 A; 1307 C; 1386 G; 1340 T; 0 U; 0 Other;
XX
Query Match 44.9%; Score 2878.4; DB 9; Length 5386;
Best local Similarity 87.3%; Pred. No. 0;
Matches 3354; Conservative 0; Mismatches 201; Indels 285; Gaps 7;
XX
QY 585 TTGAAAAAATCATGAGCATCAAAATGAAATGCAATTTATTCATATCAGATTTATCAAT 644
DB 5381 TTGAAAAAATCATGAGCATCAAAATGAAATGCAATTTATTCATATCAGATTTATCAAT 5322
QY 645 ACCATATTTTGGAAAAAGCCGTTTCTGTAATGAAGAAAGAAATCAACGAGGCAATGCA 704
DB 5321 ACCATATTTTGGAAAAAGCCGTTTCTGTAATGAAGAAAGAAATCAACGAGGCAATGCA 5262
QY 705 TAGATGCGAAGATCTGGTATCGGTCTGCGATTCGACTCGTCCAAATCAATCAAC 764
DB 5261 TAGATGCGAAGATCTGGTATCGGTCTGCGATTCGACTCGTCCAAATCAATCAAC 5202
QY 765 TATTAATTTCCCTCGTCAAAAATAGTTATCAAGTGAAGAAATCAACATGATGACGAC 824
DB 5201 TATTAATTTCCCTCGTCAAAAATAGTTATCAAGTGAAGAAATCAACATGATGACGAC 5142
QY 825 TGAATCCGATGAGATGCGAAAGCTTATGATTTCTTCCAGACTGTGTTCAACAGGCCA 884
DB 5141 TGAATCCGATGAGATGCGAAAGCTTATGATTTCTTCCAGACTGTGTTCAACAGGCCA 5082
QY 885 GCCATTAGCGTGTATCAAAATCACTGCGATCAACCAACCGTTATTCATTCGATGATG 944
DB 5081 GCCATTAGCGTGTATCAAAATCACTGCGATCAACCAACCGTTATTCATTCGATGATG 5022
QY 945 CGCTGAGGAGACGAAATAGCGATCGCTGTTAAAGGACAAATTAACAAACAGGAATCGA 1004
DB 5021 CGCTGAGGAGACGAAATAGCGATCGCTGTTAAAGGACAAATTAACAAACAGGAATCGA 4962
QY 1005 ATGCAACCGGCGGAGAAACATCTGCCAGCGCATCAACATATTTTCACTGGAATCAGAGA 1064
DB 4961 ATGCAACCGGCGGAGAAACATCTGCCAGCGCATCAACATATTTTCACTGGAATCAGAGA 4902
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OY	1065	TTCTTCTTAATACCTGGAAATGCTGTTTTTCCGGGGATGCGAGTGGTAACATGCAATC	1124
Db	4901	TTCTTCTTAATACCTGGAAATGCTGTTTTTCCGGGGATGCGAGTGGTAACATGCAATC	4842
OY	1125	ATCAGAGATACGGATAAATAATGCTTGATGGTGGAAAGAGCATAAATTCGGCAGCGTT	1184
Db	4841	ATCAGAGATACGGATAAATAATGCTTGATGGTGGAAAGAGCATAAATTCGGCAGCGTT	4782
OY	1185	TAGTGTGACCACTTCATCTGTGTAACATCATG3CAAAGCTACCTTGGCAGTTTCAGAAA	1244
Db	4781	TAGTGTGACCACTTCATCTGTGTAACATCATG3CAAAGCTACCTTGGCAGTTTCAGAAA	4722
OY	1245	CAACTGTGGCGATCGGGCTTCCCAATAAATCGATAGATTTGCACTGATGTCGCCGAC	1304
Db	4721	CAACTGTGGCGATCGGGCTTCCCAATAAATCGATAGATTTGCACTGATGTCGCCGAC	4662
OY	1305	ATTATCGGAGCCCATTTATATACCATATAAATCAGATCCATGTTGGAAATTAATCCGG	1364
Db	4661	ATTATCGGAGCCCATTTATATACCATATAAATCAGATCCATGTTGGAAATTAATCCGG	4602
OY	1365	CCTGAGCAAGACGTTTCCCGTTGAATATGCTCATTAACCCCTGTATTACTGTTAT	1424
Db	4601	CCTGAGCAAGACGTTTCCCGTTGAATATGCTCATTAACCCCTGTATTACTGTTAT	4542
OY	1425	GTAAAGCAACAGTTTATTTATTTGTCATGATGATATATTTTTATCTGTGCAATGTAACATCA	1484
Db	4541	GTAAAGCAACAGTTTATTTATTTGTCATGATGATATATTTTTATCTGTGCAATGTAACATCA	4521
OY	1485	GAGATTTTGAACAACAAAGTGGCTTTCGCCCCCTCGACAGGTTTCTTCTTTTCCC	1544
Db	4520	-----	4521
OY	1545	CACCCACCCCCCAAGTTCCGGGTGAAGGCCAAGGCTCGACCAAGTCCGGGCGGACG	1604
Db	4520	-----	4521
OY	1605	GCCCTGCATAGCCTCAGATTACTCATATATCTTATGATTGATTAAAACTTCATTTTT	1664
Db	4520	-----	4521
OY	1665	AATTTAAAGATCTAAGTGAAGATCCTTTTGATATCTCATAGCAAAAATCCCTTAAC	1724
Db	4520	-----TCATGACCAAAATCCCTTAAC	4500
OY	1725	GTGATTTTCTGTTCCACTGAGGTCAGACCCCGTAGAAATAGATCAAGATCTTCTGAG	1784
Db	4499	GTGATTTTCTGTTCCACTGAGGTCAGACCCCGTAGAAATAGATCAAGATCTTCTGAG	4440
OY	1785	ATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACAACGCTACAGCGG	1844
Db	4439	ATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACAACGCTACAGCGG	4380
OY	1845	TGCTTTGTTTGC CGGATCAAGAGCTACCAACTTTTTCGAAAGTAACTGGCTTCAGCA	1904
Db	4379	TGCTTTGTTTGC CGGATCAAGAGCTACCAACTTTTTCGAAAGTAACTGGCTTCAGCA	4320
OY	1905	GAGCGCAGATACCAAAATAGTGTCTTCTAGGTAGACCGTAGTTAGGCGCACCACTTCAGA	1964
Db	4319	GAGCGCAGATACCAAAATAGTGTCTTCTAGGTAGACCGTAGTTAGGCGCACCACTTCAGA	4260
OY	1965	ACTCTGTAGCAACGCTTACATACCTCGCTCTGTATATCTGTTCAGATG---GCTGCTG	2021
Db	4259	ACTCTGTAGCAACGCTTACATACCTCGCTCTGTATATCTGTTCAGATG---GCTGCTG	4200
OY	2022	CCAGTGGGGAATAAAGTCGTCTTACCGGGTTGGAATCAAGAAGATGTACCGGATTAAG	2081
Db	4139	CCAGTGGGGAATAAAGTCGTCTTACCGGGTTGGAATCAAGAAGATGTACCGGATTAAG	4140
OY	2082	CGACACGGTCCGGCTGAACCGAGGGGTTCTGTGCAACAGCCCAAGCTTGGAGCGAAGACT	2141
Db	4139	CGACACGGTCCGGCTGAACCGAGGGGTTCTGTGCAACAGCCCAAGCTTGGAGCGAAGACT	4080

QY	2142	ACACCGAAGTGAAGTACTCTACAGCGTGAAGCTATGAGAAAGCGCAGCGCTCCGGAAGGGA	2201
Db	4079	ACACCGAAGTGAAGTACTCTACAGCGTGAAGCTATGAGAAAGCGCAGCGCTCCGGAAGGGA	4020
QY	2202	GAAAGCGGACAGGATATCCGGTAAAGCGGACGGGTCCGAAACAGGAGACGACGAGGAGC	2261
Db	4019	GAAAGCGGACAGGATATCCGGTAAAGCGGACGGGTCCGAAACAGGAGACGACGAGGAGC	3960
QY	2262	TTCCAGGAGGGAACCGCTGGTATCTTTAATAGTCCCTGTCCGGGTTTCGGCACCTTGACTTG	2321
Db	3959	TTCCAGGAGGGAACCGCTGGTATCTTTAATAGTCCCTGTCCGGGTTTCGGCACCTTGACTTG	3900
QY	2322	AGCGTCGATTTTTGTGATGCTCCGACAGGGGGCGGACGCTATGAGAAAGCGCAGCAACG	2381
Db	3899	AGCGTCGATTTTTGTGATGCTCCGACAGGGGGCGGACGCTATGAGAAAGCGCAGCAACG	3840
QY	2382	CGGCTTTTAAACGGTTCCTGAGCTTTTGTGCGGCTTTTGTGTCACATGTTCTTCTCGT	2441
Db	3839	CGGCTTTTAAACGGTTCCTGAGCTTTTGTGCGGCTTTTGTGTCACATGTTCTTCTCGT	3780
QY	2442	TATCCCTCGATTCGTGGAATAAACCGATTAACCGC-ATGCAATAGTTAATAGTAATC	2500
Db	3779	TATCCCTCGATTCGTGGAATAAACCGATTAACCGCCTTTGATGAGTCGATACCGCTCGCC	3720
QY	2501	AATTAAGGGGCTATTAGTTCAATAGCCCAATATAGGATTCGGGTACATTAAC--TTAC	2557
Db	3719	GCACGCCAAGACCCGACGCGACGACGACGATGACGAGGAAGCGGAAGACGCGCCCAATAC	3660
QY	2558	GGTAAATGGCCCGCGCTGGCTGACCGGCCCAAGACCCCGCCATGACGTCATTAATAGAC	2617
Db	3659	GCAATCCGCTCTCCCGCGGTTGGCCGATTCATTAATGACGCTGGACGACAGGTTTC	3600
QY	2618	GAGATCTGATATAGGTGACAGACGATATGAGGCTATATCCCGATAGAGCGACATCAAG	2677
Db	3599	CCGACTGGAAGCGGAGAGTGAAGCGCAACGCAATTAATGAGGTACTCACTCATTAAG	3540
QY	2678	C-----TGGCACATGGCCCAATGCAATATGATCTAATCATTTAATTAATTTG--	2725
Db	3539	CACCCAGGCTTTACACTTATATGCTTCGGGCTGATATGTTGATGAGTGAAGCGGAT	3480
QY	2726	--CAATTAGCCATTAATGCTATTGGTTATATAGATTAATCAATATTGGCT-----ATT	2777
Db	3479	AACAATTTCAACACGGAACAGCTATACCAATGATTAATGCGCAAGCTTGCAATGCTGAGT	3420
QY	2778	GGCATTGCGATAGCTGATCTATATCATATATATGATCACTTAATATGGCTCATGTCCA	2837
Db	3419	GGCATTGCGATAGCTGATCTATATCATATATATGATCACTTAATATGGCTCATGTCCA	3360
QY	2838	TATGACCGGCATGTTGACATTGATTATGATCTAGTTATTATAGTAATCAATTAACGGGT	2897
Db	3359	CATTACCGGCATGTTGACATTGATTATGATCTAGTTATTATAGTAATCAATTAACGGGT	3300
QY	2898	CATTAGTTCAATAGCCCATATATGAGATTCCGCGTTACATTACTTAACGTTAATATGGCCCGC	2957
Db	3299	CATTAGTTCAATAGCCCATATATGAGATTCCGCGTTACATTACTTAACGTTAATATGGCCCGC	3240
QY	2958	CTGGCTGACCGCCCAAGACCCCGCCCATTTGACGTCGAATGATGAGCTATGTTCCCATAG	3017
Db	3239	CTGGCTGACCGCCCAAGACCCCGCCCATTTGACGTCGAATATGAGCTATGTTCCCATAG	3180
QY	3018	TAAAGCCAAATAGGACCTTTCATTTGACGTCGAATGAGGTGAGTATTTACGGTAAACTGCC	3077
Db	3179	TAAAGCCAAATAGGACCTTTCATTTGACGTCGAATGAGGTGAGTATTTACGGTAAACTGCC	3120
QY	3078	ACTTGGGAGTACATCAAGTGTATATATATGCCAAAGTCCGCCCTTATGACGTCAATGAC	3137
Db	3119	ACTTGGGAGTACATCAAGTGTATATATATGCCAAAGTCCGCCCTTATGAGGTCAATGACG	3060
QY	3138	GTAATATGGCCCGCTGGCATTTATGCGCAGTACATGACCTTAACGGGACTTTCTCTACTTGGC	3197
Db	3059	GTAATATGGCCCGCTGGCATTTATGCGCAGTACATGACCTTAATGGGACTTTCTCTACTTGGC	3000
QY	3198	AGTACATCTACGATTAATGATCATGCTATTAACATGATGATGCGGTTTGGCAGTACACA	3257

Db 2999 AGTACATCTAAGTATGATCGTATTACATGAGTGGCGGTTTGGCACTATCATCA 2940
Qy 3258 ATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTTCCAAGTCTCCACCCCATGAGCTCA 3317
Db 2939 ATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTTCCAAGTCTCCACCCCATGAGCTCA 2880
Qy 3318 ATGGAGTTTGTGTTGGCACAAATCAACGGGACCTTCCAAAATGTCTGAATPAACCCCG 3377
Db 2879 ATGGAGTTTGTGTTGGCACAAATCAACGGGACCTTCCAAAATGTCTGAATPAACCCCG 2820
Qy 3378 CCGCGTTAGCGCAATGGGGGTAGCGCTTACGGTGGGAGTCTATATPAAGAGAGCTC 3437
Db 2819 CCGCATTTAGCGCAATGGGGGTAGCGCTTACGGTGGGAGTCTATATPAAGAGAGCTC 2760
Qy 3438 GTTTAGTGAACCGCTAGATCGCTGGAGAGAGCCATCCACGCTGTTTGAACCTCCATAGAA 3497
Db 2759 GTTTAGTGAACCGCTAGATCGCTGGAGAGAGCCATCCACGCTGTTTGAACCTCCATAGAA 2700
Qy 3498 GACACCGGAGCCGATCCAGCTCCGCGCGGGAAACGGTGCATTGGAACGGGATTTCCC 3557
Db 2699 GACACCGGAGCCGATCCAGCTCCGCGCGGGAAACGGTGCATTGGAACGGGATTTCCC 2640
Qy 3558 GTGCGAAGAGTGAAGTAAAGTACCGGCTATAGACTCTATAGGACACCCCTTTGGCTTTA 3617
Db 2639 GTGCGAAGAGTGAAGTAAAGTACCGGCTATAGAGCTATAGGACACCCCTTTGGCTTTA 2580
Qy 3618 TGCATGCTATACGTTTGGCTTGGGGCTTATACACCCCGCTTCTTATGCTATAGT 3677
Db 2579 TGCATGCTATACGTTTGGCTTGGGGCTTATACACCCCGCTTCTTATGCTATAGT 2520
Qy 3678 GATGTATAGCTTACGCTTATAGTGTGGTTATTTAGCACTTATTTAGCACTCCCTATTTG 3737
Db 2519 GATGTATAGCTTACGCTTATAGTGTGGTTATTTAGCACTTATTTAGCACTCCCTATTTG 2460
Qy 3738 GTGACGATACCTTCCATTAATTAATCCATTAATGAGTCTTTGGCAACAATCTCTATATG 3797
Db 2459 GTGACGATACCTTCCATTAATTAATCCATTAATGAGTCTTTGGCAACAATCTCTATATG 2400
Qy 3798 GCTATATNGCCATACCTCTGCTCTTCAAGAGCTGATGCTGTTTATTTTCAAGAGT 3857
Db 2399 GCTATATNGCCATACCTCTGCTCTTCAAGAGCTGATGCTGTTTATTTTCAAGAGT 2340
Qy 3858 GGGTCCCATTTATTTATTTACAAATTCACATATACAAACGCGCTCCCGCCGCGAG 3917
Db 2339 GGGTCCCATTTATTTATTTACAAATTCACATATACAAACGCGCTCCCGCCGCGAG 2280
Qy 3918 TTTTATTTAACTATAGTGTGGATCTCCACGCGAATCTCGGGTACGTTTCCGGAATGG 3977
Db 2279 TTTTATTTAACTATAGTGTGGATCTCCACGCGAATCTCGGGTACGTTTCCGGAATGG 2220
Qy 3978 GCTCTTCTCGGATAGCGGCGGAGCTTCCACATCCGAGCCCTGGTCCCATCTCCAGCGG 4037
Db 2219 GCTCTTCTCGGATAGCGGCGGAGCTTCCACATCCGAGCCCTGGTCCCATCTCCAGCGG 2160
Qy 4038 CTGATGATGCTCGGAGCTCTCTTCTCTTACAGTGTAGGAGCCAGATTAGGACAGCAC 4097
Db 2159 CTGATGATGCTCGGAGCTCTCTTCTCTTACAGTGTAGGAGCCAGATTAGGACAGCAC 2100
Qy 4098 AATGCCCAACCAACCAAGTGTGCGGCAAGGCGCGTGGCGGTATGTGTCTGAAAA 4157
Db 2099 AATGCCCAACCAACCAAGTGTGCGGCAAGGCGCGTGGCGGTATGTGTCTGAAAA 2040
Qy 4158 TTAGCTCGAGATTTGGGCTCGACCGCTGACGAGATGAGAGCTTTAAGGACAGGAGAG 4217
Db 2039 TTAGCTCGAGATTTGGGCTCGACCGCTGACGAGATGAGAGCTTTAAGGACAGGAGAG 1980
Qy 4218 AGAAGATGACAGGAGCTGATGTTGTATTTCTGATTAAGATCAGAGGTAATCCCGTTGC 4277
Db 1979 AGAAGATGACAGGAGCTGATGTTGTATTTCTGATTAAGATCAGAGGTAATCCCGTTGC 1920
Qy 4278 GGTGCTTTAAGCGTGGAGGCGAGTGTATGCTGAGCAGTACTGTTGCTCGCGCGCGC 4337

Db 1919 GGTGCTTTAAGCGTGGAGGCGAGTGTATGCTGAGACGATCTGTTGCTCCCGCGCGC 1860
Qy 4338 CACCGACATATATAGCTGACAGACTPAACAGACTGTTCTTCATGCGGTCTTTTCTGAG 4397
Db 1859 CACCGACATATATAGCTGACAGACTPAACAGACTGTTCTTCATGCGGTCTTTTCTGAG 1800
RESULT 4
ADD35600/c
ID ADD35600 standard; DNA; 7086 BP.
XX
AC ADD35600;
XX
DT 15-JAN-2004 (first entry)
XX
DE Tricistronic eukaryotic expression vector pL249.
XX
KW Multicistronic eukaryotic expression vector; multiple protein expression;
KW simultaneous expression; viral internal ribosomal entry site; viral IRES;
KW chain terminator; transcription pause site; gene transfer;
KW DNA immunisation; gene therapy; pL190; kanamycin resistance gene;
KW cytomegalovirus; CMV promoter/enhancer; CMV intron A;
KW encephalomyocarditis virus; EMCV IRES; SV40 polyadenylation site;
KW Rous sarcoma virus; RSV promoter; rabbit beta-globin intron;
KW mRb terminator; cyclin; circular; ds.
XX
OS Chimeric.
OS Synthetic.
OS Human herpesvirus 5.
OS Encephalomyocarditis virus.
OS Simian virus 40.
OS Rous sarcoma virus.
OS Oryctolagus cuniculus.
OS Escherichia coli.
XX
PN MO2003031630-A1.
XX
XX
XX 17-APR-2003.
XX PD
XX
PF 10-OCT-2002; 2002WO-IT000646.
XX
XX
PR 12-OCT-2001; 2001TT-MI002110.
XX
XX (KERY-) KERYOS SPA.
XX
PA Fazio V, Rinaldi M, Sonzogni L, Tonon G, Oresini G;
PI WPI; 2003-393446/37.
XX
XX
XX
PT New multicistronic recombinant plasmid vectors expressing two to our
PT genes simultaneously, useful in various biotechnological applications,
PT such as gene transfer, gene therapy and in DNA immunisation.
XX
PS Claim 18; SEQ ID NO 3; 52pp; English.
XX
XX The invention relates to multicistronic eukaryotic expression vectors for
CC the expression of at least two proteins of interest which may be
CC identical or different. The vectors comprise at least one eukaryotic
CC expression cassette having a promoter/enhancer sequence, an intron
CC sequence, a cloning site, a viral internal ribosomal entry site (IRES)
CC and a chain terminator. The vectors may additionally contain a
CC transcription pause site downstream of the chain terminator. The
CC invention also encompasses eukaryotic host cells comprising a vector of
CC the invention, and the recombinant expression of two or more eukaryotic
CC proteins using host cells transformed with a vector of the invention.
CC The vectors are useful in various biotechnological applications in which
CC the simultaneous expression of two or more genes is necessary, such as
CC gene transfer protocols, DNA immunisation, or for the expression of
CC different molecules in the same cell. They may also be used in gene
CC therapy. The present sequence represents a specifically claimed vector
CC designated pL249, which comprises a cytomegalovirus (CMV)
CC promoter/enhancer, CMV intron A, the encephalomyocarditis virus (EMCV)
CC IRES, an SV40 polyadenylation site, a transcription pause site, a Rous

OS Hepatitis C virus.
XX Escherichia coli.
PN WO2003031630-A1.
XX 17-APR-2003.
PF 10-OCT-2002; 2002MO-IT000646.
XX 12-OCT-2001; 2001IT-MI002110.
PR (KERY-) KERYOS SPA.
XX
XX
PI Fezio V, Rinaldi M, Sonzogni L, Tonon G, Orsini G;
DR WPI; 2003-393446/37.
XX
XX
PT New multicistronic recombinant plasmid vectors expressing two to our
PT genes simultaneously, useful in various biotechnological applications,
PT such as gene transfer, gene therapy and in DNA immunization.
XX
XX
PS Claim 18; SEQ ID NO 4; 52pp; English.
XX
XX The invention relates to multicistronic eukaryotic expression vectors for
CC the expression of at least two proteins of interest which may be
CC identical or different. The vectors comprise at least one eukaryotic
CC expression cassette having a promoter/enhancer sequence, an intron
CC sequence, a cloning site, a viral internal ribosomal entry site (IRES)
CC and a chain terminator. The vectors may additionally contain a
CC transcription pause site downstream of the chain terminator. The
CC invention also encompasses eukaryotic host cells comprising a vector of
CC the invention, and the recombinant expression of two or more eukaryotic
CC proteins using host cells transfected with a vector of the invention.
CC The vectors are useful in various biotechnological applications in which
CC the simultaneous expression of two or more genes is necessary, such as
CC gene transfer protocols, DNA immunisation, or for the expression of
CC different molecules in the same cell. They may also be used in gene
CC therapy. The present sequence represents a specifically claimed vector
CC designated pL250, which comprises a cytomegalovirus (CMV)
CC promoter/enhancer, CMV intron A, the cytomagalovirus virus (CMV)
CC IRES, an SV40 polyadenylation site, a transcription pause site, a Rous
CC sarcoma virus (RSV) promoter, rabbit beta-globin intron, the hepatitis C
CC virus (HCV) IRES, and a rabbit beta-globin gene mRB terminator as well
CC as a Kanamycin resistance gene.
XX
XX
SQ Sequence 7334 BP; 1922 A; 1775 C; 1825 G; 1812 T; 0 U; 0 Other;
Query Match 44.9%; Score 2878.4; DB 9; Length 7334;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 3354; Conservative 0; Mismatches 201; Indels 285; Gaps 7;

Db 7029 GCCATTACGCTGTCATCAAAATCACTCGCATCAACCAACCGTTATTGTCGTGATTG 6970
Qy 945 CGCTGAGGAGAGCGAAATACGGATCGCTGTTAAAAAGCAATTACAAACAGGAATCGA 1004
Db 6969 CGCTGAGGAGAGCGAAATACGGATCGCTGTTAAAAAGCAATTACAAACAGGAATCGA 6910
Qy 1005 ATGCAACCGGCGAGGAAACGCGAGCGCATCAACAAATTTTCCGTAATCAGGATA 1064
Db 6909 ATGCAACCGGCGAGGAAACGCGAGCGCATCAACAAATTTTCCGTAATCAGGATA 6850
Qy 1065 TTCCTTAATACCTGGAATGCTGTTTCCGCGGATCGAGTGTGATTAACCATGATC 1124
Db 6849 TTCCTTAATACCTGGAATGCTGTTTCCGCGGATCGAGTGTGATTAACCATGATC 6790
Qy 1125 ATCAGAGTACGATTAATATGCTTGAATGTCGGAAGGATTAATTTCCGTCAGCGATT 1184
Db 6789 ATCAGAGTACGATTAATATGCTTGAATGTCGGAAGGATTAATTTCCGTCAGCGATT 6730
Qy 1185 TAGCTGACCATCTCATCTGTACATCAATTGGCAAGCTACTTTGCGATGTTCAAAA 1244
Db 6729 TAGCTGACCATCTCATCTGTACATCAATTGGCAAGCTACTTTGCGATGTTCAAAA 6670
Qy 1245 CAACTGCGGCGATCGGCGCTTCCCATCAATCGATGATTGCGACTGATTGCCGAC 1304
Db 6669 CAACTGCGGCGATCGGCGCTTCCCATCAATCGATGATTGCGACTGATTGCCGAC 6610
Qy 1305 ATTATGCGAGCCCATTTATATCCATATAATAGATTCATGTTGAATTAATGCGCG 1364
Db 6609 ATTATGCGAGCCCATTTATATCCATATAATAGATTCATGTTGAATTAATGCGCG 6550
Qy 1365 CTTGAGCAAGAGCTTCCCGTGAATATGCGTCATTAACCCCTGTATTACTGTTAT 1424
Db 6549 CTTGAGCAAGAGCTTCCCGTGAATATGCGTCATTAACCCCTGTATTACTGTTAT 6490
Qy 1425 GTAGAGAGAGCTTATTGTTATGATGATATATTTTATCTTGCAATGTAATCA 1484
Db 6489 GTAGAGAGAGCTTATTGTTATGATGATATATTTTATCTTGCAATGTAATCA 6469
Qy 1485 GAGATTTTGAGACAAACGTGCTTCCCGGCGAGCGTTCTTCTTTTCCC 1544
Db 6468 ----- 6469
Qy 1545 CACCCACCCCGCAAGTGGGTGAAGGCCAGGCTCGAGCCAACTGCGGGCGGAG 1604
Db 6468 ----- 6469
Qy 1605 GCCCTGACATGCTCAGGTTACTATATCTTATGATTGATTTAAACTTCATTTTT 1664
Db 6468 ----- 6469
Qy 1665 AATTAAAAAGATCTAGGTGAAGATCCTTTTGATATCTCATGACCAAAATCCTTAAC 1724
Db 6468 -----TCATGACCAAAATCCTTAAC 6448
Qy 1725 GTAGATTTGCTTCACTGAGGCTCAAGCCCGTGAAGAAAGATCAAGATCTTTTGAG 1784
Db 6447 GTAGATTTGCTTCACTGAGGCTCAAGCCCGTGAAGAAAGATCAAGATCTTTTGAG 6388
Qy 1785 ATCTTTTCTTGTGCGGTATCTGCTGCTTGTGAACAAAAAAACACACGCTCAAGCG 1844
Db 6387 ATCTTTTCTTGTGCGGTATCTGCTGCTTGTGAACAAAAAAACACACGCTCAAGCG 6328
Qy 1845 TGGTTTGTGTCGCGATCAAGAGCTCAACCTTTTTCGAAGATTACTGAGCTTACGA 1904
Db 6327 TGGTTTGTGTCGCGATCAAGAGCTCAACCTTTTTCGAAGATTACTGAGCTTACGA 6268
Qy 1905 GAGCGAGATACCAATATCTGCTTCTAGTGAAGCGTATGAGGCAACCACTTCAAGA 1964
Db 6267 GAGCGAGATACCAATATCTGCTTCTAGTGAAGCGTATGAGGCAACCACTTCAAGA 6208
Qy 1965 ACTCTGTAGACCGCTTACATCCTGCTCTGTAACTCTGTTACAGATG---GCTGCTG 2021
Db 6207 ACTCTGTAGACCGCTTACATCCTGCTCTGTAACTCTGTTACAGATG---GCTGCTG 6148

QY 2022 CCAAGTGGCGATTAAGTCGTGTCCTTACCGGGTTGGACTTCAGACGATTAACCGGATPAGG 2081
| | | | |
Db 6147 CCAAGTGGCGATTAAGTCGTGTCCTTACCGGGTTGGACTTCAGACGATTAACCGGATPAGG 6088
| | | | |
QY 2082 CGAGCGGTGGGCTGAACGGGGGGTTCGTGCAACAAGCCGACCTTGGAGCGAACGACT 2141
| | | | |
Db 6087 CGAGCGGTGGGCTGAACGGGGGGTTCGTGCAACAAGCCGACCTTGGAGCGAACGACT 6028
| | | | |
QY 2142 ACACCGAATGAGATACCTTACAGCGTGAAGCTATGAGAAACGCGACGCTTCCGAAAGGA 2201
| | | | |
Db 6027 ACACCGAATGAGATACCTTACAGCGTGAAGCTATGAGAAACGCGACGCTTCCGAAAGGA 5968
| | | | |
QY 2202 GAAAGCGGACAGGTATCCCGGTAAACGGGCGAGGCTCGGACAGAGAGCGACGAGGAGC 2261
| | | | |
Db 5967 GAAAGCGGACAGGTATCCCGGTAAACGGGCGAGGCTCGGACAGAGAGCGACGAGGAGC 5908
| | | | |
QY 2262 TTCACAGGGGGAACCGCTGTATCTTTATAGTCTGTGCGGGTTTCGCACTTCTGACTTG 2321
| | | | |
Db 5907 TTCACAGGGGGAACCGCTGTATCTTTATAGTCTGTGCGGGTTTCGCACTTCTGACTTG 5848
| | | | |
QY 2322 AGCGTCGATTTTGTGATGCTGTCAGAGGGGGCGAGACTATGGAAGAAACGCCAGCAAG 2381
| | | | |
Db 5847 AGCGTCGATTTTGTGATGCTGTCAGAGGGGGCGAGACTATGGAAGAAACGCCAGCAAG 5788
| | | | |
QY 2382 CGGCTTTTTCAGGTTCTGAGCTTGTGCTGGCTTTTGTCTCAATGTTCTTTCTGCGT 2441
| | | | |
Db 5787 CGGCTTTTTCAGGTTCTGAGCTTGTGCTGGCTTTTGTCTCAATGTTCTTTCTGCGT 5728
| | | | |
QY 2442 TATCCCTGATTTCTGAGATTAACCGTATTAACCGCC-ATGCAATAGTTATTAATAGTATC 2500
| | | | |
Db 5727 TATCCCTGATTTCTGAGATTAACCGTATTAACCGCTTGTAGTAGAGTAAACCGCTGCC 5668
| | | | |
QY 2501 AATTACGGGGTCAATTAGTTCATAGCCCATATATATGAGTTCCGGTTTACATTAAC- 2557
| | | | |
Db 5667 GCAGCCGAACGACCGAGCGAGCGAGTCAAGTGAACGAGAGAGAGAGAGCGCCCAATAC 5608
| | | | |
QY 2558 GGTAAATGCGCGCTGCTGACCGCCCAAGACCCCGCCCATTTGACGTCATTAATGAC 2617
| | | | |
Db 5607 GCAAAACGCGCTCTCCCGCGGTTGGCGAATTCATTAATGACGTGACGACGAGGTTTC 5548
| | | | |
QY 2618 GAATCTGATATAGTGAACAAGATATGAGGCTATATCGCCATTAAGAGCGACATTAAG 2677
| | | | |
Db 5547 CCGACTGGAAGCGGGGAGTGAAGCGCAACCAATTAATGATGATGACTCACTCATTAAG 5488
| | | | |
QY 2678 C-----TGGCATGAGCCAAATGATCATGATCATATACATTAATGATGCT-----ATT 2725
| | | | |
Db 5487 CACCCAGGCTTACACTTATGCTTCCGCTGATATGTTGTGGAATTTGTGAGCGGAT 5428
| | | | |
QY 2726 --CAATTAGCCATATTAAGTCATGTTATATATAGCATTAATCAATTAATGCT-----ATT 2777
| | | | |
Db 5427 AACAAATTCACACGAGAAACAGCATATGACCATTAATGACGCAAGCTTGCAATGCTGAGT 5368
| | | | |
QY 2778 GGGCATTTGCAATGCTTAT 2837
| | | | |
Db 5367 GGGCATTTGCAATGCTTAT 5308
| | | | |
QY 2838 TATGACCGGACATGTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2897
| | | | |
Db 5307 CATTACGCGCATGTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5248
| | | | |
QY 2898 CATTAGTTCATAGCCCAT 2957
| | | | |
Db 5247 CATTAGTTCATAGCCCAT 5188
| | | | |
QY 2958 CTGGCTGACCGCCCAAGACCGCCCGCCCATTTGACGTCATATGATGATGATGATGATGATG 3017
| | | | |
Db 5187 CTGGCTGACCGCCCAAGACCGCCCGCCCATTTGACGTCATATGATGATGATGATGATGATG 5128
| | | | |
QY 3018 TAAAGCCATTAAGGAGCTTTCATATTAATGATGATGATGATGATGATGATGATGATGATGATG 3077
| | | | |
Db 5127 TAAAGCCATTAAGGAGCTTTCATATTAATGATGATGATGATGATGATGATGATGATGATGATG 5068
| | | | |

QY 3078 ACTTGCGAGTACATCAAGTATATATATGCAAGTCCGCCCTATATGACGTCAATGACG 3137
| | | | |
Db 5067 ACTTGCGAGTACATCAAGTATATATATGCAAGTCCGCCCTATATGACGTCAATGACG 5008
| | | | |
QY 3138 GTTAAATGCGCGCTGCGCATTAATGCGCGATATATATATATATATATATATATATATATATAT 3197
| | | | |
Db 5007 GTTAAATGCGCGCTGCGCATTAATGCGCGATATATATATATATATATATATATATATATATAT 4948
| | | | |
QY 3198 AGTACATCTACGATTAATGATCATGCTATTAATGATGATGATGATGATGATGATGATGATGATG 3257
| | | | |
Db 4947 AGTACATCTACGATTAATGATCATGCTATTAATGATGATGATGATGATGATGATGATGATGATG 4888
| | | | |
QY 3258 ATGCGCGTGAATGCGGTTTGAATCAAGGGAATTTCAAGTCTCCACCCCATTTGACGTCA 3317
| | | | |
Db 4887 ATGCGCGTGAATGCGGTTTGAATCAAGGGAATTTCAAGTCTCCACCCCATTTGACGTCA 4828
| | | | |
QY 3318 ATGCGGATTTGTTTGGGCAACCAATCAAGGGAATTTCAAGTCTCCAAATGCTGATTAACCCCG 3377
| | | | |
Db 4827 ATGCGGATTTGTTTGGGCAACCAATCAAGGGAATTTCAAGTCTCCAAATGCTGATTAACCCCG 4768
| | | | |
QY 3378 CCCGTTGACGCAATGCGCGGTAAGCGGTGTAACGTTGAGAGGTCATATATAGCAGAGCTC 3437
| | | | |
Db 4767 CCCGTTGACGCAATGCGCGGTAAGCGGTGTAACGTTGAGAGGTCATATATAGCAGAGCTC 4708
| | | | |
QY 3438 GTTTAGTGAACGTCAGATGCGCTGAGACGCCATTCACGCTGTTTGAACCTTCATAGAA 3497
| | | | |
Db 4707 GTTTAGTGAACGTCAGATGCGCTGAGACGCCATTCACGCTGTTTGAACCTTCATAGAA 4648
| | | | |
QY 3498 GACACCGGGAACGATCAACCTCCGCGCGGGAACGGGCAATGGAAGCGGGAATTCGCC 3557
| | | | |
Db 4647 GACACCGGGAACGATCAACCTCCGCGCGGGAACGGGCAATGGAAGCGGGAATTCGCC 4588
| | | | |
QY 3558 GTGCAAGAGTGAACGTAAATGACCGCTATATAGCTATAGGACACCCCTTTGGCTCTTA 3617
| | | | |
Db 4587 GTGCAAGAGTGAACGTAAATGACCGCTATATAGCTATAGGACACCCCTTTGGCTCTTA 4528
| | | | |
QY 3618 TGCATCTATACCTGTTTGGCTTGGGCTTATATACCCCCGCTTCTATATAGT 3677
| | | | |
Db 4527 TGCATCTATACCTGTTTGGCTTGGGCTTATATACCCCCGCTTCTATATAGT 4468
| | | | |
QY 3678 GATGATATAGCTTAAGCTATATAGTGGTATTAATGACATTAATGACACTCCCATATG 3737
| | | | |
Db 4467 GATGATATAGCTTAAGCTATATAGTGGTATTAATGACATTAATGACACTCCCATATG 4408
| | | | |
QY 3738 GTGACGATCTTTCATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 3797
| | | | |
Db 4407 GTGACGATCTTTCATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 4348
| | | | |
QY 3798 GCTAATGCGCAATCTCTGCTCTTCAAGAGCTGAACAAGGACTCTGATTTTTCACAGATG 3857
| | | | |
Db 4347 GCTAATGCGCAATCTCTGCTCTTCAAGAGCTGAACAAGGACTCTGATTTTTCACAGATG 4288
| | | | |
QY 3858 GGGTCCATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3917
| | | | |
Db 4287 GGGTCCATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4228
| | | | |
QY 3918 TTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3977
| | | | |
Db 4227 TTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4168
| | | | |
QY 3978 GCTCTTCTCCGGAAGCGGCGAGCTTCAATCCGAGCCCTGCTCCATGCTCCAGCGG 4037
| | | | |
Db 4167 GCTCTTCTCCGGAAGCGGCGAGCTTCAATCCGAGCCCTGCTCCATGCTCCAGCGG 4108
| | | | |
QY 4038 CTCATGCTGCTCGGAGGCTCTGCTCTTAACAGTGAAGGCGAGCTTAAGGCAAGCAGCAG 4097
| | | | |
Db 4107 CTCATGCTGCTCGGAGGCTCTGCTCTTAACAGTGAAGGCGAGCTTAAGGCAAGCAGCAG 4048
| | | | |
QY 4098 AATGCCACCAACCAACGATGTCGCGCAAGGCGGCTGAGGATATGATGATGATGATGATGATG 4157
| | | | |
Db 4047 AATGCCACCAACCAACGATGTCGCGCAAGGCGGCTGAGGATATGATGATGATGATGATGATG 3988
| | | | |
QY 4158 TGAAGTCGAGATTTGGGCTCGACCGCTGACGCAAGTGAAGACTTAAAGCAGCGGACAG 4217
| | | | |

Db 3987 TGAGCGTGGAGATGGGCTCCGACGCTGACGAGATGGAAGACTTAAGCAGCGCAGA 3928
 Qy 4218 AGAAGATGACGAGCAGCTGAGTGTGTATTCGTATTAAGAGTCAAGAGGTAATCCGTTGC 4277
 Db 3927 AGAAGATGACGAGCAGCTGAGTGTGTATTCGTATTAAGAGTCAAGAGGTAATCCGTTGC 3868
 Qy 4278 GGTGCTGTAAACGGTGGAGGGCAGTGTAGTCTAGACAGTACTCCTTGTCTGCCGCGC 4337
 Db 3867 GGTGCTGTAAACGGTGGAGGGCAGTGTAGTCTAGACAGTACTCCTTGTCTGCCGCGC 3808
 Qy 4338 CACACAGCATTAATAGTGAAGAGTAAACAGACTGTTCCCTTGCATGGGCTCTTTCTGAC 4397
 Db 3807 CACACAGCATTAATAGTGAAGAGTAAACAGACTGTTCCCTTGCATGGGCTCTTTCTGAC 3748
 RESULT 6
 AB259287
 ID AB259287 standard; DNA; 5089 BP.
 AC AB259287;
 DT 10-MAY-2003 (first entry)
 XX
 DE Plasmid pPUV2003 SEQ ID NO 2.
 XX
 KW ADP-ribosylating exotoxin; immune response; immunisation; vaccine;
 KW adjuvant; cholera toxin subunit B; CTB; human cytomegalovirus; hCMV;
 KW human tissue plasminogen activator; circular; cyclic; de.
 XX
 OS Synthetic.
 XX
 PN MO200304055-A2.
 PD 16-JAN-2003.
 XX
 PF 26-NOV-2001; 2001MO-US043151.
 XX
 PR 27-NOV-2000; 2000US-00724315.
 XX
 PA (POMD-) POMDERJECT VACCINES INC.
 XX
 PI Haynes JR, Arrington JE;
 DR WPI; 2003-221541/21.
 XX
 PT New compositions comprising nucleic acid adjuvants, useful in
 PT immunization techniques, particularly for eliciting or enhancing an
 PT immune response against an antigen in a human.
 XX
 PS Example 1; Fig 2; 143p; English.
 XX
 CC The invention relates to a composition comprising: (a) a first nucleic
 CC acid sequence that is a truncated A subunit coding region obtained or
 CC derived from a bacterial ADP-ribosylating exotoxin; and (b) a second
 CC nucleic acid sequence that is a truncated B subunit coding region
 CC obtained or derived from a bacterial ADP-ribosylating exotoxin. Each of
 CC the truncated subunit coding regions has a 5' deletion and encodes a
 CC subunit peptide not having an amino terminal bacterial signal peptide.
 CC The composition is useful for eliciting an immune response against an
 CC antigen or for manufacturing a medicament for enhancing an immune
 CC response in a vertebrate subject (specifically a human) against an
 CC antigen. The composition is particularly useful as nucleic acid adjuvants
 CC for use in immunisation techniques. The present sequence is that of a
 CC plasmid expression vector that contains a truncated coding sequence for a
 CC cholera toxin (CT) subunit B (CTB) peptide, the human cytomegalovirus
 CC (hCMV) immediate early promoter and associated intron A sequence and the
 CC coding sequence for the signal peptide of human tissue plasminogen
 CC activator, to allow for secretion from mammalian cells of the truncated
 CC CTB expression product
 XX
 SQ Sequence 5089 BP; 1268 A; 1260 C; 1267 G; 1294 T; 0 U; 0 other;

Query Match 37.1%; Score 2378.8; DB 7; Length 5089;
 Best Local Similarity 91.6%; Pred. No. 0;
 Matches 2598; Conservative 0; Mismatches 197; Indels 41; Gaps 6;
 Qy 1615 AGCCTGAGTTACTCATATATATTAATTAAGATTTAAATTAATTTAAATTTAAAG 1674
 Db 1067 AGACCAAGTTTACTCATATATTAATTAAGATTTAAATTAATTTAAATTTAAAG 1126
 Qy 1675 GATCTAGTGAAGATCTTTTGTATTAATCTATGACCAAAATCCCTTAAGTGAATTTTC 1734
 Db 1127 GATCTAGTGAAGATCTTTTGTATTAATCTATGACCAAAATCCCTTAAGTGAATTTTC 1186
 Qy 1735 GTTCCACTGAGCGTCAAGACCCGTAAGAAAGATCAAGAGATCTTCTTGAGATCTTTTTC 1794
 Db 1187 GTTCCACTGAGCGTCAAGACCCGTAAGAAAGATCAAGAGATCTTCTTGAGATCTTTTTC 1246
 Qy 1795 TCTGCGGTATCTGCTGTGTAACCAAAAAACACGCTTCAAGCGTGTGTTGTTT 1854
 Db 1247 TCTGCGGTATCTGCTGTGTAACCAAAAAACACGCTTCAAGCGTGTGTTGTTT 1306
 Qy 1855 GCCGATCAAGAGCTACCACTCTTTTCCGAAGTAACTGCTTCAAGAGCGCAGAT 1914
 Db 1307 GCCGATCAAGAGCTACCACTCTTTTCCGAAGTAACTGCTTCAAGAGCGCAGAT 1366
 Qy 1915 ACCAATATCTGTTCTCTAGTGTAGCGGTAGTAAAGCAGACCTTCAAGAACTCTGAGC 1974
 Db 1367 ACCAATATCTGTTCTCTAGTGTAGCGGTAGTAAAGCAGACCTTCAAGAACTCTGAGC 1426
 Qy 1975 ACCGCTCAATATCTGCTGTGTAACCTGTTACGAGTGGTGTCTCCAGTGGCGATAA 2034
 Db 1427 ACCGCTCAATATCTGCTGTGTAACCTGTTACGAGTGGTGTCTCCAGTGGCGATAA 1486
 Qy 2035 GTGCTGTCTTAACCGGGTTGAGCTCAAGACGATAGTTACCGATTAAGCGCAGCGTCCGG 2094
 Db 1487 GTGCTGTCTTAACCGGGTTGAGCTCAAGACGATAGTTACCGATTAAGCGCAGCGTCCGG 1546
 Qy 2095 CTGAACGGGGGTTTCGTGCAACAGCCCACTTGGAGCGCAAGACCTTCAACCGAATCGAG 2154
 Db 1547 CTGAACGGGGGTTTCGTGCAACAGCCCACTTGGAGCGCAAGACCTTCAACCGAATCGAG 1606
 Qy 2155 ATACTCAAGCGTGAAGTATGAAGAAAGCGCAGCTTCCGAAAGGAGAAAGCGCAGAG 2214
 Db 1607 ATACTCAAGCGTGAAGTATGAAGAAAGCGCAGCTTCCGAAAGGAGAAAGCGCAGAG 1666
 Qy 2215 GTATCCGTAAGCGGACGGGTGCGAACAGGAGCGCAGAGGAGCTTCCAGGGGAGAA 2274
 Db 1667 GTATCCGTAAGCGGACGGGTGCGAACAGGAGCGCAGAGGAGCTTCCAGGGGAGAA 1726
 Qy 2275 CGCTGATATCTTATATAGTCTGTCCGGTTTCCCACTTGAAGGTGATTTT 2334
 Db 1727 CGCTGATATCTTATATAGTCTGTCCGGTTTCCCACTTGAAGGTGATTTT 1786
 Qy 2335 GTGATGCTGTCAAGGGGGGCGAGCGTATGAAAGAAAGCGCAGAAACGCGGCTTTTACG 2394
 Db 1787 GTGATGCTGTCAAGGGGGGCGAGCGTATGAAAGAAAGCGCAGAAACGCGGCTTTTACG 1846
 Qy 2395 GTTCTGAGCTTTTGTGCTTGTGCTTGTCAATGTTCTTCTGCGTTATCCCTGATTC 2454
 Db 1847 GTTCTGAGCTTTTGTGCTTGTGCTTGTGCTCAATGTTCTTCTGCGTTATCCCTGATTC 1906
 Qy 2455 TGTGATTAACCGTATTAACCGCATGCTATGTTATTAATGTATATC-----ATTA 2505
 Db 1907 TGTGATTAACCGTATTAACCGCATGCTATGTTATTAATGTATATC-----ATTA 1966
 Qy 2506 CGGGGATTAATGTTTCAATAGCCCATTAATGAGAGTTCCGCTTAATTAATTAAGTAAATG 2565
 Db 1967 CGAGCGAGGAGATCTAGTACGAGAAAGCGGAGAGCGCCCAATACGCAACCGCTCT 2026
 Qy 2566 GCCCGCTGTGCTAGCGCCCAAGACGCCCGCCCATTAATGATCAATTAATGACGAG---- 2620
 Db 2027 CCCCGCGCTGTGCGCATTAATGACGCTGCGACAGAGGTTTCCCATGCTGAAAGC 2086
 Qy 2621 -----ATCGATTAATGATGAGAGAGATTAATGAGGCTATATCG 2657

PR 27-NOV-2000; 2000US-00724315.
XX
XX (POMD-) POMDERJECT VACCINES INC.
XX
XX Haynes JR, Arrington JE,
XX
XX WPI; 2003-221541/21.
DR
XX
XX
PT New compositions comprising nucleic acid adjuvants, useful in
PT immunization techniques, particularly for eliciting or enhancing an
PT immune response against an antigen in a human.
XX
XX Example 2; Fig 5; 143pp; English.
XX
XX The invention relates to a composition comprising: (a) a first nucleic
XX acid sequence that is a truncated A subunit coding region obtained or
XX derived from a bacterial ADP-ribosylating exotoxin; and (b) a second
XX nucleic acid sequence that is a truncated B subunit coding region
XX obtained or derived from a bacterial ADP-ribosylating exotoxin. Each of
XX the truncated subunit coding regions has a 5' deletion and encodes a
XX subunit peptide not having an amino terminal bacterial signal peptide.
XX The composition is useful for eliciting an immune response against an
XX antigen or for manufacturing a medicament for enhancing an immune
XX response in a vertebrate subject (specifically a human) against an
XX antigen. The composition is particularly useful as nucleic acid adjuvants
XX for use in immunisation techniques. The present sequence is that of a
XX plasmid expression vector that contains a truncated coding sequence for
XX an E. coli heat labile enterotoxin (LT) subunit B (LTB) peptide, the
XX human cytomegalovirus (hCMV) immediate early promoter and associated
XX intron A sequence and the coding sequence for the signal peptide of human
XX tissue plasminogen activator, to allow for secretion from mammalian cells
XX of the truncated LTB expression product
SQ Sequence 5089 BP; 1270 A; 1273 C; 1267 G; 1279 T; 0 U; 0 Other;

Query March 37.1%; Score 2378.8; DB 7; Length 5089;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 2598; Conservative 0; Mismatches 197; Indels 41; Gaps 6;

QY 1615 AGCCTCAGTCTACTCATATATATCTTAGATTGATTTAAACTGATTTTAAATTAAAG 1674
DB 1067 AGACCAAGTTTACTCATATATATCTTAGATTGATTTAAACTGATTTTAAATTAAAG 1126
QY 1675 GATCTAGGTGAAGATCTCTTTTGAATATCTCATGACCAAAATCCCTTACGCTGATTTTC 1734
DB 1127 GATCTAGGTGAAGATCTCTTTTGAATATCTCATGACCAAAATCCCTTACGCTGATTTTC 1186
QY 1735 GTTCCACGTGAGCGTCAGACCCCGTAGAAAGATCAAGAGATCTCTTGAGATCCTTTTTC 1794
DB 1187 GTTCCACGTGAGCGTCAGACCCCGTAGAAAGATCAAGAGATCTCTTGAGATCCTTTTTC 1246
QY 1795 TCTGCGGTATCTGCTGCTTGCAACAAAAACAACCGCTACACGCGGTGTTGTTT 1854
DB 1247 TCTGCGGTATCTGCTGCTTGCAACAAAAACAACCGCTACACGCGGTGTTGTTT 1306
QY 1855 GCGGATCTAAGAGCTACCAACTCTTTTCCGAAGGTAACTGCTTCACAGAGCGCAGAT 1914
DB 1307 GCGGATCTAAGAGCTACCAACTCTTTTCCGAAGGTAACTGCTTCACAGAGCGCAGAT 1366
QY 1915 ACCGAAATCTGTTTCTTAAGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTTAGC 1974
DB 1367 ACCGAAATCTGTTTCTTAAGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTTAGC 1426
QY 1975 ACCGCTACATACCTGCTCTGCTAATCTGTATCCAGTGAGCTGCTGCGAGTGAAT 2034
DB 1427 ACCGCTACATACCTGCTCTGCTAATCTGTATCCAGTGAGCTGCTGCGAGTGAAT 1486
QY 2035 GTGCTGTTTACCGGGTTGACTCAAGACGATAGTTACCGGATTAAGCGCGCGCTGCGG 2094
DB 1487 GTGCTGTTTACCGGGTTGACTCAAGACGATAGTTACCGGATTAAGCGCGCGCTGCGG 1546
QY 2095 CTGAAGCGGGGGTTCGTGACACAGCCAGCTTGAGAGGAACGATCAACCGAATCGAG 2154

DB 1547 CTGAAGCGGGGGTTCGTGACACAGCCAGCTTGAGAGGAACGATCAACCGAATCGAG 1606
QY 2155 ATACCTACAGCGGTGAGCTATGAGAAAGCGGCACAGCTTCCGAAAGGAGAAAGCGGACAG 2214
DB 1607 ATACCTACAGCGGTGAGCTATGAGAAAGCGGCACAGCTTCCGAAAGGAGAAAGCGGACAG 1666
QY 2215 GTATCCGGTAAAGCGGCGAGGGTCCGAAACAGAGACGCAAGAGGAGCTTCAGAGGAGAA 2274
DB 1667 GTATCCGGTAAAGCGGCGAGGGTCCGAAACAGAGACGCAAGAGGAGCTTCAGAGGAGAA 1726
QY 2275 CGCCTGGTATCTTATATAGTCTGTGCGGTTTCGCAACCTTCGACTGAGAGCGATTTT 2334
DB 1727 CGCCTGGTATCTTATATAGTCTGTGCGGTTTCGCAACCTTCGACTGAGAGCGATTTT 1786
QY 2335 GTGATGCTGCTCAGGGGGGCGAGGCTATGAGAAAGCGGCACAGCGGCTTTTACG 2394
DB 1787 GTGATGCTGCTCAGGGGGGCGAGGCTATGAGAAAGCGGCACAGCGGCTTTTACG 1846
QY 2395 GTTCCGCGCTTTTGTGCGGCTTTTGTCAACATGTTCTTCCGCGTATCCCTGATTC 2454
DB 1847 GTTCCGCGCTTTTGTGCGGCTTTTGTCAACATGTTCTTCCGCGTATCCCTGATTC 1906
QY 2455 TGTGATTAACCGTATTACCGCCATGATTAATTATTATATC-----AATTA 2505
DB 1907 TGTGATTAACCGTATTACCGCCATGATTAATTATTATATC-----AATTA 1966
QY 2506 CGGGGTCTATTAGTTCAATAGCCATATATATGAGTTCCGCTTACATTAATTAGGTAATG 2565
DB 1967 CGAGCCAGAGGATCAGTAGAGCAGAGAAAGCGGCAATCGCAAAACCGCTCT 2026
QY 2566 GCCCGCTGCTGACCGCCCAAGACCCCGCCCATTTGAGCTCAATATATGACGAG----- 2620
DB 2027 CCCCGCGCTTGTGCGGCTTATTAATGACGCTGCGACGAGGTTCCGACGTGAAAGC 2086
QY 2621 -----ATCGATATATGAGTACGAGATGAGCTATATG 2657
DB 2087 GGGCAGTGAAGCGACGACGATTAATGAGTTAGTCACTCATTAAGCACCCAGGCTT 2146
QY 2658 CGGATNAGAGCGACATCAAGCTGCGACATGCGCAATGATGATCATATGATATC 2717
DB 2147 ACACTTATATGCTTCCGCTGATGTTGTGAGAAATGAGCGGATTAACATTTACAC 2206
QY 2718 AATATGGAATTAAGCATTAATGATGATGATGATTAATAGATTAATCAATATGCGTAT 2777
DB 2207 AGGAAACAGCTATGACCATGATTAATGACCAAGCTGACATATTAATCAATATGCGTAT 2266
QY 2778 GGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2837
DB 2267 GGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2326
QY 2838 TATGACCGCATGTTGACATTTGATTAATGATTAATGATTAATGATTAATGATTAATGAT 2897
DB 2327 TATGACCGCATGTTGACATTTGATTAATGATTAATGATTAATGATTAATGATTAATGAT 2386
QY 2898 CATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 2957
DB 2387 CATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 2446
QY 2958 CTGGCTGACCGGCCAAGACCGCCCGCATGACGCAATGATGAGGATGATGATGATGATGAT 3017
DB 2447 CTGGCTGACCGGCCAAGACCGCCCGCATGACGCAATGATGAGGATGATGATGATGATGAT 2505
QY 3018 TAAAGCCATTAAGGACCTTTCATTTGACGTCATGAGGTGAGTATTAACGGTAAATGCGCC 3077
DB 2506 TAAAGCCATTAAGGACCTTTCATTTGACGTCATGAGGTGAGTATTAACGGTAAATGCGCC 2565
QY 3078 ACTTGGAGATGATCAAGTATGATCAATGATGATGATGATGATGATGATGATGATGATGAT 3136
DB 2566 ACTTGGAGATGATCAAGTATGATCAATGATGATGATGATGATGATGATGATGATGATGAT 2625
QY 3137 GGTAAATGCGCGCTGAGCATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 3196
DB 2626 GGTAAATGCGCGCTGAGCATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 2685

QY 3197 CAGTACATCTACGATATAGTCAATGCTATTACCATGGTGTGATGGGTTTGGCAGTACACC 3256
 DB 2686 CAGTACATCTACGATATAGTCAATGCTATTACCATGGTGTGATGGGTTTGGCAGTACACC 2745
 QY 3257 AATGGCGGTGGATAGCGGTTTGAAGTCAAGGGGATTTCCAAAGTCTCCACCCCATTTGAGCTC 3316
 DB 2746 AATGGCGGTGGATAGCGGTTTGAAGTCAAGGGGATTTCCAAAGTCTCCACCCCATTTGAGCTC 2805
 QY 3317 AATGGGAGTTTGTTTGGCACCACCAAAATCAACGGGACTTTCCAAAATGTCGTAATTAACCC 3376
 DB 2806 AATGGGAGTTTGTTTGGCACCACCAAAATCAACGGGACTTTCCAAAATGTCGTAATTAACCC 2865
 QY 3377 GCCCGCTTGAACGCAAAATGGCGGTGAGCGTACGCTGAGAGGCTTATATAGCAGAGCT 3436
 DB 2866 GCCCGCTTGAACGCAAAATGGCGGTGAGCGTACGCTGAGAGGCTTATATAGCAGAGCT 2925
 QY 3437 CGTTTATGTAACCGTCAAGATCCCTTGAAGACCCATCAAGCTGTTTGTACCTTCATAGA 3496
 DB 2926 CGTTTATGTAACCGTCAAGATCCCTTGAAGACCCATCAAGCTGTTTGTACCTTCATAGA 2985
 QY 3497 AGACACCGGGACCGATCCAGCTCCGCGCGGGGAAAGGTGCAATGGAGCGGGAATCCC 3556
 DB 2986 AGACACCGGGACCGATCCAGCTCCGCGCGGGGAAAGGTGCAATGGAGCGGGAATCCC 3045
 QY 3557 CGTCCCAAGAGTACGTAAGTACCGCTTATAGACTCTATAGGCAACACCCCTTGGCTCTT 3616
 DB 3046 CGTCCCAAGAGTACGTAAGTACCGCTTATAGACTCTATAGGCAACACCCCTTGGCTCTT 3105
 QY 3617 ATGCAATGCTAATCTGTTTGGCTGGGGCTTATAGACCCCGCTTCTTATGCTATAGG 3676
 DB 3106 ATGCAATGCTAATCTGTTTGGCTGGGGCTTATAGACCCCGCTTCTTATGCTATAGG 3164
 QY 3677 TGATGATATAGCTTAGGCTTATAGGTGGTGTGATTTAGCACTTATGACCACTCCCTATT 3736
 DB 3165 TGATGATATAGCTTAGGCTTATAGGTGGTGTGATTTAGCACTTATGACCACTCCCTATT 3224
 QY 3737 GGTGACGATACCTTCCATTAATAATCAATCAATGAGCTCTTGGCAGCAACTATCTATT 3796
 DB 3225 GGTGACGATACCTTCCATTAATAATCAATGAGCTCTTGGCAGCAACTATCTATT 3284
 QY 3797 GGTATATGCAATATCTCTCTTCAAGACTGACACGAGCTCTGATTTTTCACAGAT 3856
 DB 3285 GGTATATGCAATATCTCTCTTCAAGACTGACACGAGCTCTGATTTTTCACAGAT 3344
 QY 3857 GGGGTCCCATTTTATTTCAAAATCAATCAATCAATGAGCTCTTGGCAGCAACTATCTATT 3916
 DB 3345 GGGGTCCCATTTTATTTCAAAATCAATCAATCAATGAGCTCTTGGCAGCAACTATCTATT 3404
 QY 3917 GTTTTATTAACATGAGCGTGGGATCTCAACGCGAATCTCGGGTACGTTTCCGAGCATG 3976
 DB 3405 GTTTTATTAACATGAGCGTGGGATCTCAACGCGAATCTCGGGTACGTTTCCGAGCATG 3464
 QY 3977 GGTCTTCTCCGGTGAAGCGGAGCTTCCATCCGAGCTTCCATGCTTCCAGCG 4036
 DB 3465 GGTCTTCTCCGGTGAAGCGGAGCTTCCATCCGAGCTTCCATGCTTCCAGCG 3524
 QY 4037 GGTCAATGATGCTGCGAGGCTCTTGTCTTAAAGAGGAGGAGGAGCTTATAGGACAGCA 4096
 DB 3525 GGTCAATGATGCTGCGAGGCTCTTGTCTTAAAGAGGAGGAGGAGCTTATAGGACAGCA 3584
 QY 4097 CAATGCCACCAACCAACAGTGTGCGCAAGAGCGGTGAGGATATGCTGTGAAA 4156
 DB 3585 CAATGCCACCAACCAACAGTGTGCGCAAGAGCGGTGAGGATATGCTGTGAAA 3644
 QY 4157 ATGAGCTCGGAGATTTGGCTTGCACCGCTGACGAGATGGAAGCTTAAAGGACGCGGAG 4216
 DB 3645 ATGAGCTCGGAGATTTGGCTTGCACCGCTGACGAGATGGAAGCTTAAAGGACGCGGAG 3703
 QY 4217 AAGAGATGAGGAGGAGCTGATGTTGATTTCTGATAGAGTCAAGAGTAACTCCGCTG 4276
 DB 3704 AAGAGATGAGGAGGAGCTGATGTTGATTTCTGATAGAGTCAAGAGTAACTCCGCTG 3763

QY 4277 CCGTCTGTTAAACGTTGAGGCGAGTGTAGTCTGACAGTACTCGTTGCTGCCGCGCG 4336
 DB 3764 CCGTCTGTTAAACGTTGAGGCGAGTGTAGTCTGACAGTACTCGTTGCTGCCGCGCG 3823
 QY 4337 CCACGAGCATATATAGCTGACAGACTGAACAGCTGTTCTTCCATGGGCTTTTCTGCA 4396
 DB 3824 CCACGAGCATATATAGCTGACAGACTGAACAGCTGTTCTTCCATGGGCTTTTCTGCA 3883
 QY 4397 GTCAACCTGCAAGCGCT 4412
 DB 3884 GTCAACCTGCAAGCTT 3899
 RESULT 8
 ABZ59291
 ID ABZ59291 standard; DNA; 5488 BP.
 XX
 AC ABZ59291;
 XX
 DT 10-MAY-2003 (first entry)
 XX
 DE Plasmid pPUV2006 SEQ ID NO 6.
 XX
 KW ADP-ribosylating exotoxin; immune response; immunisation; vaccine;
 KW adjuvant; labile enterotoxin subunit A; LTA; human cytomegalovirus; hCMV;
 KW human tissue plasminogen activator; circular; cyclic; ds.
 XX
 OS Synthetic.
 XX
 PN WO2003004055-A2.
 XX
 PD 16-JAN-2003.
 XX
 PF 26-NOV-2001; 2001WO-US043151.
 XX
 PR 27-NOV-2000; 2000US-00724315.
 XX
 XX (POMD-) POWDERJECT VACCINES INC.
 XX PA Haynes JR, Arrington JE;
 XX PI
 XX
 DR WPI; 2003-221541/21.
 XX
 XX
 PT New compositions comprising nucleic acid adjuvants, useful in
 PT immunization techniques, particularly for eliciting or enhancing an
 PT immune response against an antigen in a human.
 PS Example 2; Fig 6; 143pp; English.
 XX
 XX The invention relates to a composition comprising: (a) a first nucleic
 CC acid sequence that is a truncated A subunit coding region obtained or
 CC derived from a bacterial ADP-ribosylating exotoxin; and (b) a second
 CC nucleic acid sequence that is a truncated B subunit coding region
 CC obtained or derived from a bacterial ADP-ribosylating exotoxin. Each of
 CC the truncated subunit coding regions has a 5' deletion and encodes a
 CC subunit peptide not having an amino terminal bacterial signal peptide.
 CC The composition is useful for eliciting an immune response against an
 CC antigen or for manufacturing a medicament for enhancing an immune
 CC response in a vertebrate subject (specifically a human) against an
 CC antigen. The composition is particularly useful as nucleic acid adjuvants
 CC for use in immunisation techniques. The present sequence is that of a
 CC plasmid expression vector that contains a truncated coding sequence for
 CC an E. coli heat labile enterotoxin (LT) subunit A (LTA) peptide with a
 CC deletion of the C-terminal RDEL motif, the human cytomegalovirus (hCMV)
 CC immediate early promoter and associated intron A sequence and the coding
 CC sequence for the signal peptide of human tissue plasminogen activator, to
 CC allow for secretion from mammalian cells of the truncated LTA expression
 CC product
 XX
 SQ 'Sequence 5488 BP; 1381 A; 1339 C; 1362 G; 1406 T; 0 U; 0 Other;
 Query Match 37.1%; Score 2378.8; DB 7; Length 5488;
 Best Local Similarity 91.6%; Pred. No. 0;

Matches 2598; Conservative 0; Mismatches 197; Indels 41; Gaps 6;

QY 1615 AGCCTCAGGTTACTCATATATATCTTGAATGATTAAACTTATTTTAAATTAAG 1674
DB |||||
DB 1067 AGACCAAGTTTACTCATATATATCTTGAATGATTAAACTTATTTTAAATTAAG 1126
QY 1675 GATCTAGGTAAGATCTTTTGTATATCATGACCAAAATCCCTTAAGGTGTTTC 1734
DB |||||
DB 1127 GATCTAGGTAAGATCTTTTGTATATCATGACCAAAATCCCTTAAGGTGTTTC 1186
QY 1735 GTTCACTGAGCGCTCAGACCCCGTAGAAAGATCAAGATCTTCTGAGATCTTTT 1794
DB |||||
DB 1187 GTTCACTGAGCGCTCAGACCCCGTAGAAAGATCAAGATCTTCTGAGATCTTTT 1246
QY 1795 TCTGCGGTATCTGCTGCTTGCAACAAAAACAACCGTACACGCGGTGTTTGT 1854
DB |||||
DB 1247 TCTGCGGTATCTGCTGCTTGCAACAAAAACAACCGTACACGCGGTGTTTGT 1306
QY 1855 GCGGAGCAAGAGTACCAACTCTTTTCCGAAGTATGCTGCTTCAAGAGCGAGAT 1914
DB |||||
DB 1307 GCGGAGCAAGAGTACCAACTCTTTTCCGAAGTATGCTGCTTCAAGAGCGAGAT 1366
QY 1915 ACCAATATCTGTTCTTCTAGTAGCGGTAGTGGCCACACTTCAAGAACTGTAGC 1974
DB |||||
DB 1367 ACCAATATCTGTTCTTCTAGTAGCGGTAGTGGCCACACTTCAAGAACTGTAGC 1426
QY 1975 ACCGCTTACATACCTGCTCTGCTAATCTGTTTCAAGTGGCTGCTCCAGTGGCAT 2034
DB |||||
DB 1427 ACCGCTTACATACCTGCTCTGCTAATCTGTTTCAAGTGGCTGCTCCAGTGGCAT 1486
QY 2035 GTGCTGCTTACCGGGGTGAGCTCAAGACATAGTTACCGGATTAAGCGCGGTGGG 2094
DB |||||
DB 1487 GTGCTGCTTACCGGGGTGAGCTCAAGACATAGTTACCGGATTAAGCGCGGTGGG 1546
QY 2095 CTGAACGGGGGGTCTGTGACACACAGCCAGCTTGGAGGAAAGCACTTACCGAATGAG 2154
DB |||||
DB 1547 CTGAACGGGGGGTCTGTGACACACAGCCAGCTTGGAGGAAAGCACTTACCGAATGAG 1606
QY 2155 ATATCTTACAGCGTGAAGTATGAGAAAGCGCCAGCTTCCCGAAGGAGAAAGCGGACAG 2214
DB |||||
DB 1607 ATATCTTACAGCGTGAAGTATGAGAAAGCGCCAGCTTCCCGAAGGAGAAAGCGGACAG 1666
QY 2215 GTATCCGCTAAGCGCGGCTCGAACAAGAGACGCAAGGAGGAGCTTCAAGGGGAAA 2274
DB |||||
DB 1667 GTATCCGCTAAGCGCGGCTCGAACAAGAGACGCAAGGAGGAGCTTCAAGGGGAAA 1726
QY 2275 CGCCTGATCTTATATAGTCTGTGCGGGTTTCCGCACTTGAATTGAGCGTCAATTTT 2334
DB |||||
DB 1727 CGCCTGATCTTATATAGTCTGTGCGGGTTTCCGCACTTGAATTGAGCGTCAATTTT 1786
QY 2335 GTGATGCTCGTCAAGGGGGGCGAGCCTATGGAAGAAAGCGCAAGCGCGCTTTTACG 2394
DB |||||
DB 1787 GTGATGCTCGTCAAGGGGGGCGAGCCTATGGAAGAAAGCGCAAGCGCGCTTTTACG 1846
QY 2395 GTTCTGAGCTTTTGTGCTGCTTTTGTCTCAATGTTCTTCTGCTTATCCCTGATTC 2454
DB |||||
DB 1847 GTTCTGAGCTTTTGTGCTGCTTTTGTCTCAATGTTCTTCTGCTTATCCCTGATTC 1906
QY 2455 TGTGATTAACCGTATACCGCATGATGATTAATTAATAGTATC-----AATTA 2505
DB |||||
DB 1907 TGTGATTAACCGTATACCGCATGATGATTAATTAATAGTATC-----AATTA 1966
QY 2506 CGGGGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2565
DB |||||
DB 1967 CGAAGCGAGCGAGTCAAGTGAAGCGAGAAAGCGAAGAGCGCAATTAAGCAAAACGCGCTCT 2026
QY 2566 GCGCGCTGAGTCAAGTGAAGCGAGAAAGCGAAGAGCGCAATTAAGCAAAACGCGCTCT 2620
DB |||||
DB 2027 CCGCGCGCTTGGCGGATCTTAATGAGCTGCGACGACGAGTTTCCCGACTGGAAGC 2086
QY 2621 -----ATCTGATTAAGGTGACAGACGATTAAGGAGTTCG 2657
DB |||||
DB 2087 GGGAGTGAAGCGCAACGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2146

QY 2658 CCGATAGAGCGGACATCAAGCTGGCACATGGCCCAATGCAATGATCTATACATGAATC 2717
DB |||||
DB 2147 ACACCTTAATGCTTCGCGCTCGTATGTTGTGGAATTTGAGCGGATTAACAAATTTACAC 2206
QY 2718 AATATTGGCAATTAAGCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2777
DB |||||
DB 2207 AGGAACAGCTATGACCATATATATGACCAAGCTAAGTGAACATTAATTAATTAATTAAT 2266
QY 2778 GGCATTTGATGAGTGTAT 2837
DB |||||
DB 2267 GGCATTTGATGAGTGTAT 2326
QY 2838 TATGACCGCATATGATGAT 2897
DB |||||
DB 2327 TATGACCGCATATGATGAT 2386
QY 2898 CATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2957
DB |||||
DB 2387 CATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2446
QY 2958 CTGCTGACCGCCCAACGACCCCGCCCATTTGACGTCAATGATGACGTATGTTCCATAG 3017
DB |||||
DB 2447 CTGCTGACCGCCCAACGACCCCGCCCATTTGACGTCAATGATGACGTATGTTCCATAG 2505
QY 3018 TAAAGCCATAGGAGCTTTTCAATGACGTCAATGAGGTGAGATTTTAAACGTAAATGCC 3077
DB |||||
DB 2506 TAAAGCCATAGGAGCTTTTCAATGACGTCAATGAGGTGAGATTTTAAACGTAAATGCC 2565
QY 3078 ACTTGGAGATGATCAAGTGTATCATATGCAAGTGC -GCCCTTATGACGTCAATGAC 3136
DB |||||
DB 2566 ACTTGGAGATGATCAAGTGTATCATATGCAAGTGC -GCCCTTATGACGTCAATGAC 2625
QY 3137 GGTAAATGCGCCCTGCGCATTAATGCGCAATGACCTTACGGAATTTCTACTTGG 3196
DB |||||
DB 2626 GGTAAATGCGCCCTGCGCATTAATGCGCAATGACCTTACGGAATTTCTACTTGG 2685
QY 3197 CAGTACATCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3256
DB |||||
DB 2686 CAGTACATCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2745
QY 3257 AATGGGCGGTGATGAGGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3316
DB |||||
DB 2746 AATGGGCGGTGATGAGGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2805
QY 3317 AATGGGCGGTGATGAGGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3376
DB |||||
DB 2806 AATGGGCGGTGATGAGGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2865
QY 3377 GCCCGCTTGAAGCAATGGGCGGTGATGATGATGATGATGATGATGATGATGATGATGAT 3436
DB |||||
DB 2866 GCCCGCTTGAAGCAATGGGCGGTGATGATGATGATGATGATGATGATGATGATGATGAT 2925
QY 3437 CGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3496
DB |||||
DB 2926 CGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2985
QY 3497 AGACACCGGAGCGATCAAGCTCCGCGCGCGGAAAGCGTGAATGGAACGCGAATTC 3556
DB |||||
DB 2986 AGACACCGGAGCGATCAAGCTCCGCGCGCGGAAAGCGTGAATGGAACGCGAATTC 3045
QY 3557 CGTGCACAGTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3616
DB |||||
DB 3046 CGTGCACAGTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3105
QY 3617 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3676
DB |||||
DB 3106 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3164
QY 3677 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3736
DB |||||
DB 3165 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3224

QY 2155 ATACCTACAGCGTAGCTATGAGAAAGCCACGCTTCCCGAAGGAGAAAGCGGACAG 2214
Db 1607 ATACTCTACAGCGTAGCTATGAGAAAGCCACGCTTCCCGAAGGAGAAAGCGGACAG 1666
QY 2215 GTATCCCGTAAGCGGAGCGGTCCGAAACGAGAGACGCGAGGAGCTTCCAGGGGAGAA 2274
Db 1667 GTATCCCGTAAGCGGAGCGGTCCGAAACGAGAGACGCGAGGAGCTTCCAGGGGAGAA 1726
QY 2275 CGCTGTATCTTTATATAGTCTGTCCGGTTTCGACCTCTGACTTGAAGCGTCGATTTT 2334
Db 1727 CGCTGTATCTTTATATAGTCTGTCCGGTTTCGACCTCTGACTTGAAGCGTCGATTTT 1786
QY 2335 GTATGTCTCTGACAGGGGGGCGGAGCTTATGAAAAAGCCAGCAACCGGCTTTTACG 2394
Db 1787 GTATGTCTCTGACAGGGGGGCGGAGCTTATGAAAAAGCCAGCAACCGGCTTTTACG 1846
QY 2395 GTTCTGGGCTTTTGTGCGGCTTTTGTGCACATGTTCTTTCTGCTGTTATCCCTGATTC 2454
Db 1847 GTTCTGGGCTTTTGTGCGGCTTTTGTGCACATGTTCTTTCTGCTGTTATCCCTGATTC 1906
QY 2455 TGTGATTAACCGTAATTAACCGCATGCAATTAGTTATTAATGATTC-----AATTA 2505
Db 1907 TGTGATTAACCGTAATTAACCGCATGCAATTAGTTATTAATGATTC-----AATTA 1966
QY 2506 CGGGGTATTAGTTCAATAGCCCATATATAGAGTTCCGCTTACATTAAGTTAATG 2565
Db 1967 CGAGCGAGCGAGTCAAGTAGACGAGAAAGCGGAGAGCGCCAAATAGCAACCGCTCT 2026
QY 2566 GCCCGCTGTGCTAGCGCCCAAGACCCCGCCATTGAGGTCAATATAGCGAG----- 2620
Db 2027 CCCCCGCGTTTGGCCGATTCAATTAATGAGCTGGACGACAGGTTTCCCGACTGGAAGC 2086
QY 2621 -----ATCTATATAGTTGACAGACGATATGAGGCTATATCG 2657
Db 2087 GGGCAGTAGAGCGCAACGCAATTAATGAGTTAGCTCACTTAAGGACCCCGGCTTT 2146
QY 2658 CCGATTAAGCGGCAATCAAGCTGGCAATGCGCCATGCAATGCAATCAATTAATG 2717
Db 2147 ACACCTTATATGCTTCCGCTCGTATGTTGTGTGAAATGTGAGCGGATTAACATTTCCAC 2206
QY 2718 AATATGCGCAATGAGCATATTAGTCAATGCTTATATAGCAATATGCAATATGCGCAT 2777
Db 2207 AGGAAACAGCTATACCAATGATTAAGCCAAAGCTAGTGAACAAATATGATGCTATT 2266
QY 2778 GGCATTGCAATACGTTGATCTATATCATATATATATGATCAATTAATGCTCATGCCAA 2837
Db 2267 GGCATTGCAATACGTTGATCTATATCATATATATGATCAATTAATGCTCATGCCAA 2326
QY 2838 TATGACCGCCATGTTGACATGATTATGACTAGTTAATATGATTAATCAATTAAGGGGT 2897
Db 2327 TATACCGCCCATGTTGACATGATTATGACTAGTTAATATGATTAATCAATTAAGGGGT 2386
QY 2898 CATATGTTCAATAGCCCATATATGAGTTCCGCTTACATTAAGTAAATGCGCCG 2957
Db 2387 CATATGTTCAATAGCCCATATATGAGTTCCGCTTACATTAAGTAAATGCGCCG 2446
QY 2958 CTGCTGACCGCCCAAGCAACCCCGCCCATGAGCGTCAATGATGACGTTATGCCATAG 3017
Db 2447 CTGCTGACCGCCCAAGCAACCCCGCCCATGAGCGTCAATGATGACGTTATGCCATAG 2505
QY 3018 TAAAGCCCAATAGGACCTTTGATGAGTCAATGAGTGGTGGAGTATTACGTTAACTGCC 3077
Db 2506 TAAAGCCCAATAGGACCTTTGATGAGTCAATGAGTGGTGGAGTATTACGTTAACTGCC 2565
QY 3078 ACTTGGAGTATCAATCAAGTGTATATATAGCCAGTCC-GCCCGCTATGAGCGTAAAGAC 3136
Db 2566 ACTTGGAGTATCAATCAAGTGTATATATAGCCAGTCCGCGCCCTATGAGCGTAAAGAC 2625
QY 3137 GGTAAATGCGCGCTGGCATTTATGCCAGTATCAATGACCTTACGGAATTTCTTACTTGG 3196
Db 2626 GGTAAATGCGCGCTGGCATTTATGCCAGTATCAATGACCTTACGGAATTTCTTACTTGG 2685

QY 3197 CAGTACATCTAGCTATTATAGTCAATGCTGCTATTACCATGAGTATGCGGTTTTGGACATACCC 3256
Db 2686 CAGTACATCTAGCTATTATAGTCAATGCTGCTATTACCATGAGTATGCGGTTTTGGACATACCC 2745
QY 3257 AATGGCGTGTATAGCGGTTTGAATCAAGGGGATTTTCAAGTCTCAACCCCATTTGACGTC 3316
Db 2746 AATGGCGTGTATAGCGGTTTGAATCAAGGGGATTTTCAAGTCTCAACCCCATTTGACGTC 2805
QY 3317 AATGGGAGTTGTTTTGGACCAAAATCAAGGGGATTTTCAAAATGTCGTAATTAACCC 3376
Db 2806 AATGGGAGTTGTTTTGGACCAAAATCAAGGGGATTTTCAAAATGTCGTAATTAACCC 2865
QY 3377 GCCCGGTGACGAAATGGCGGTAGCGGTACGCTGAGGAGGCTATATAAAGAGCT 3436
Db 2866 GCCCGGTGACGAAATGGCGGTAGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCT 2925
QY 3437 CGTTTATGTAACCGTCAATCGCTGAGACGCGCATCAAGCTGTTTTGACCTCATAGA 3496
Db 2926 CGTTTATGTAACCGTCAATCGCTGAGACGCGCATCAAGCTGTTTTGACCTCATAGA 2985
QY 3497 AGACACCGGACCGATCCAGCTCCGCGCGCGGAAAGCGTGCATTGGAACGCGGATTC 3556
Db 2986 AGACACCGGACCGATCCAGCTCCGCGCGCGGAAAGCGTGCATTGGAACGCGGATTC 3045
QY 3557 CGTGCAGAGTGAAGTAAAGTACCGGCTATAGACTGATAGGACACCCCTTGGGCTCT 3616
Db 3046 CGTGCAGAGTGAAGTAAAGTACCGGCTATAGACTGATAGGACACCCCTTGGGCTCT 3105
QY 3617 ATGCATGCTATCTGTTTTGGCTTGGGCGCTTATACCCCGCTTCTTATGCTATAG 3676
Db 3106 ATGCATGCTATCTGTTTTGGCTTGGGCGCTTATACCCCGCTTCTTATGCTATAG 3164
QY 3677 TGAATGTAATGCTTAAGCTATAGTGTGGTTATTAACATTAATGAACAATCCCTAT 3736
Db 3165 TGAATGTAATGCTTAAGCTATAGTGTGGTTATTAACATTAATGAACAATCCCTAT 3224
QY 3737 GGTGAGATATCTTTCCATTAATCAATCAATGCTGCTTTTCCCAATATCTAT 3796
Db 3225 GGTGAGATATCTTTCCATTAATCAATCAATGCTGCTTTTCCCAATATCTAT 3284
QY 3797 GGTATATGCAATATCTGCTCTTCAAGAGCTGACAGGACTGATATTTTACAGAT 3856
Db 3285 GGTATATGCAATATCTGCTCTTCAAGAGCTGACAGGACTGATATTTTACAGAT 3344
QY 3857 GGGGTCCCATTTATTTTCAAAATCAATATCAATATCAACAAAGCGCTGCTCCGCGCA 3916
Db 3345 GGGGTCCCATTTATTTTCAAAATCAATATCAATATCAACAAAGCGCTGCTCCGCGCA 3404
QY 3917 GTTTTATTTAAATAGCGGTGATCTCCAGCGGAATCTCGGTAAGTGTCCGGAATG 3976
Db 3405 GTTTTATTTAAATAGCGGTGATCTCCAGCGGAATCTCGGTAAGTGTCCGGAATG 3464
QY 3977 GGTCTTCTCCGCTAGCGGCGAGCTTCCATCCGAGCCCTGATCCCATGCTCCAGCG 4036
Db 3465 GGTCTTCTCCGCTAGCGGCGAGCTTCCATCCGAGCCCTGATCCCATGCTCCAGCG 3524
QY 4037 GCTCATAGTGTGCTCGGAGCTCTCTGCTCTTAACAGTGAAGGCAAGACTTAAGCAACGA 4096
Db 3525 GCTCATAGTGTGCTCGGAGCTCTCTGCTCTTAACAGTGAAGGCAAGACTTAAGCAACGA 3584
QY 4097 CAATGCCCAACACACAGTGTGCGCAAAAGGCGTGGGTAGGGTATGTGCTGAAA 4156
Db 3585 CAATGCCCAACACACAGTGTGCGCAAAAGGCGTGGGTAGGGTATGTGCTGAAA 3644
QY 4157 ATGAGCTCGAGATTTGGGCTCGACCGCTGACCGAGTGAAGACTTAAGGAGCGGAG 4216
Db 3645 ATGAGCTCGAGATTTGGGCTCGACCGG-TGACCGAATGGAABAATTAAGGAGCGGAG 3703
QY 4217 AAGAAATGCAAGCAAGTGTGTTGATTTGATTAAGAGTCAAGAGTAACTCCGTTG 4276
Db 3704 AAGAAATGCAAGCAAGTGTGTTGATTTGATTAAGAGTCAAGAGTAACTCCGTTG 3763
QY 4277 CGGTGCTGTTAAAGGTGAGGGGAGTGTAGTCTGAGCAGTAACTGTTGCTGCGCGGCG 4336

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|||||
Db      3764  CGGTGCTGTTAAACGGTGAAGGCGAGTGTAGTCTGACACAGTACGTGTGCTGCGCGCGG 3823
QY      4337  CCACGACGACATTAATACCTGACAGACTAACGACTGTTCCCTTCATGGGCTTTTCTGCA 4396
Db      3824  CCACGACGACATTAATACCTGACAGACTAACGACTGTTCCCTTCATGGGCTTTTCTGCA 3883
QY      4397  GTCACCGTCCACGCGT 4412
Db      3884  GTCACCGTCCACGCTT 3899

RESULT 10
ABZ59289
ID      ABZ59289 standard; DNA; 5500 BP.
XX
XX      ABZ59289;
AC
XX      10-MAY-2003 (first entry)
XX
XX      Plasmid pPUV2004 SEQ ID NO 4.
DE
XX      ADP-ribosylating exotoxin; immune response; immunisation; vaccine;
KM      adjuvant; labile enterotoxin subunit A; LTA; human cytomegalovirus; hCMV;
KW      human tissue plasmidogen activator; circular; cyclic; ds.
XX
XX      Synthetic.
OS
XX      MO2003004055-A2.
PN
XX      16-JAN-2003.
PD
XX      26-NOV-2001; 2001MO-US043151.
PF
XX      27-NOV-2000; 2000US-00724315.
PR
XX      (POWD-) POWDERJECT VACCINES INC.
PA
XX      Haynes JR, Arrington JE;
PI
XX      WPI; 2003-221541/21.
DR
XX
XX      New compositions comprising nucleic acid adjuvants, useful in
PT      immunization techniques, particularly for eliciting or enhancing an
PT      immune response against an antigen in a human.
XX
XX      Example 2; Fig 4; 143pp; English.
PS
XX
XX      The invention relates to a composition comprising: (a) a first nucleic
CC      acid sequence that is a truncated A subunit coding region obtained or
CC      derived from a bacterial ADP-ribosylating exotoxin; and (b) a second
CC      nucleic acid sequence that is a truncated B subunit coding region
CC      obtained or derived from a bacterial ADP-ribosylating exotoxin. Each of
CC      the truncated subunit coding regions has a 5' deletion and encodes a
CC      subunit peptide not having an amino terminal bacterial signal peptide.
CC      The composition is useful for eliciting an immune response against an
CC      antigen or for manufacturing a medicament for enhancing an immune
CC      response in a vertebrate subject (specifically a human) against an
CC      antigen. The composition is particularly useful as nucleic acid adjuvants
CC      for use in immunisation techniques. The present sequence is that of a
CC      plasmid expression vector that contains a truncated coding sequence for
CC      an E. coli heat labile enterotoxin (LT) subunit A (LTA) peptide, the
CC      human cytomegalovirus (hCMV) immediate early promoter and associated
CC      intron A sequence and the coding sequence for the signal peptide of human
CC      tissue plasmidogen activator, to allow for secretion from mammalian cells
CC      of the truncated LTA expression product
CC
XX
SQ      Sequence 5500 BP; 1385 A; 1340 C; 1367 G; 1408 T; 0 U; 0 Other;
Query Match      37.1%; Score 2378.8; DB 7; Length 5500;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 2596; Conservative 0; Mismatches 197; Indels 41; Gaps 6;
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Db 2147 ACACTTATGCTTCGGGCTGCTATGTTGTGTGGAAATGTGAGCGGATTAACAATTTTCACAC 2206
Qy 2718 AATATTTGGCAATTAAGCCATATTTAGTCATTTGGTTATATAGCATTAATATATTTGGCTATTT 2777
Db 2207 AGGAAAAGGCTATGACCATGATTTACGCCAAGCTAGTCGACATAAATCAATTTGGCTATTT 2266
Qy 2778 GGGCATTGCACTGTTGATCTATATCATATAATATGTAATTTATTTATTTGGCTCATATGCCAA 2837
Db 2267 GGGCATTGCACTGTTGATCTATATCATATAATATGTAATTTATTTATTTGGCTCATATGCCAA 2326
Qy 2838 TATGACCGCCATGTTGACATTTGATTTATTTAGTATTTAATATTTAGTATTTAGTATTTAGT 2897
Db 2227 TATATCCGCCATGTTGACATTTGATTTATTTAGTATTTAATATTTAGTATTTAGTATTTAG 2386
Qy 2898 CATTAGTTCAATAGCCCATATATATGAGTTCCGCGTTACATTAATTACGTTAATATGAGCCGC 2957
Db 2287 CATTAGTTCAATAGCCCATATATATGAGTTCCGCGTTACATTAATTACGTTAATATGAGCCGC 2446
Qy 2958 CTGGCTGACCGCCCAAGACCCCGCCCATTTGACGTCAATGATGAGTATGTTCCCATAG 3017
Db 2447 CTCG-TGACCGCCCAAGACCCCGCCCATTTGACGTCAATGATGAGTATGTTCCCATAG 2505
Qy 3018 TTAAGCCCAATAGGACCTTTCCATTTAGTCAATGAGTCAATGAGTATTTAAGGTTAACTGCCC 3077
Db 2506 TTAAGCCCAATAGGACCTTTCCATTTAGTCAATGAGTCAATGAGTATTTAAGGTTAACTGCCC 2565
Qy 3078 ACTTGGACATACATCAAGTATATATATGCAAGTCC-GCCCGCTATTTGACGTCAATGAC 3136
Db 2566 ACTTGGACATACATCAAGTATATATATGCAAGTCCGCGCCCGCTATTTGACGTCAATGAC 2625
Qy 3137 GGTAAATGCGCCGCTGCTGATTTATGCGCAGTACATGACCTTTACGCGGACTTTCTACTTGG 3196
Db 2626 GGTAAATGCGCCGCTGCTGATTTATGCGCAGTACATGACCTTTACGCGGACTTTCTACTTGG 2685
Qy 3197 CAGTACATCTACGATTTATGATATGCTATTTACATGAGTATGAGTATTTGACATGAC 3256
Db 2686 CAGTACATCTACGATTTATGATATGCTATTTACATGAGTATGAGTATTTGACATGAC 2745
Qy 3257 AATGGGCGTGAATAGCGGTTTGTCACTCAAGGGAATTTCCAAAGTCTCCACCATTGAGCTC 3316
Db 2746 AATGGGCGTGAATAGCGGTTTGTCACTCAAGGGAATTTCCAAAGTCTCCACCATTGAGCTC 2805
Qy 3317 AATGGAGTTTGTGTTGGCACAAATTCACGCGGACTTTCCAAATGTCGTAATTAACCC 3376
Db 2806 AATGGAGTTTGTGTTGGCACAAATTCACGCGGACTTTCCAAATGTCGTAATTAACCC 2865
Qy 3377 GCGCCGTTGACGCAATGAGGCGGTAGGCGTGTACGCTGAGGAGTCTATATTAAGCAGAGCT 3436
Db 2866 GCGCCGTTGACGCAATGAGGCGGTAGGCGTGTACGCTGAGGAGTCTATATTAAGCAGAGCT 2925
Qy 3437 CGTTTATGTAACCGTCAGATCGCTGAGAGCGCCATCCAGCTGTTTGTGACCTTCATAGA 3496
Db 2926 CGTTTATGTAACCGTCAGATCGCTGAGAGCGCCATCCAGCTGTTTGTGACCTTCATAGA 2985
Qy 3497 AGACACCGGAGCCGATCCAGCTCCGCGCCGAGGACGCTGATTTGAAACCGGATTTCC 3556
Db 2986 AGACACCGGAGCCGATCCAGCTCCGCGCCGAGGACGCTGATTTGAAACCGGATTTCC 3045
Qy 3557 CGTCCCAAGAGTACGTAAGTACGCGCTATATGATCTCTATTAAGGACACCCCTTTGGCTTT 3616
Db 3046 CGTCCCAAGAGTACGTAAGTACGCGCTATATGATCTCTATTAAGGACACCCCTTTGGCTTT 3105
Qy 3617 ATGATGCTATACGTTTGTGCTTGGGCTTATATACACCCCGCTTCCTTATGCTATAGG 3676
Db 3106 ATGATGCTATACGTTTGTGCTTGGGCTTATATACACCCCGCTTCCTTATGCTATAGG 3164
Qy 3677 TGATGTAATAGCTTATAGCTATATAGTGTGCTTATTTAGCACTATTTAGCACTCCCTATTT 3736
Db 3165 TGATGTAATAGCTTATAGCTTATATAGTGTGCTTATTTAGCACTATTTAGCACTCCCTATTT 3224
Qy 3737 GGTACGATACTTTCCATTAATCAATACATGAGCTTTGACAGCACTATCTATTT 3796

Db 3225 GGTACGATACCTTCCATTAATCAATACATGAGCTTTTSCCAAACTATCTCATTT 3284
Qy 3797 GGTATATGCAATACCTCTGCTCTTCAAGACCTGACACGAGCTCTGATTTTAAACGAT 3856
Db 3285 GGTATATGCAATACCTCTGCTCTTCAAGACCTGACACGAGCTCTGATTTTAAACGAT 3344
Qy 3857 GGGGTCCTATTTATTTATTAACAATCAATATACATATACAAACGCGCTCCCGGCGCA 3916
Db 3345 GGGGTCCTATTTATTTATTAACAATCAATATACATATACAAACGCGCTCCCGGCGCA 3404
Qy 3917 GTTTTATTAACAATACATGCGGTGATCTCCACGCGAATCTTCGGTACGTTTCCGACATG 3976
Db 3405 GTTTTATTAACAATACATGCGGTGATCTCCACGCGAATCTTCGGTACGTTTCCGACATG 3464
Qy 3977 GGTCTTCTCCGCTAGCGCGGAGCTTTCCACATCCGAGCCCTGCTCCATGCTCCAGCG 4036
Db 3465 GGTCTTCTCCGCTAGCGCGGAGCTTTCCACATCCGAGCCCTGCTCCATGCTCCAGCG 3524
Qy 4037 GGTCTATGCTGCTCCGCGAGCTCTTGTCTCTCTAACAATGAGGAGGACGACCTTAAGGCA 4096
Db 3525 GGTCTATGCTGCTCCGCGAGCTCTTGTCTCTCTAACAATGAGGAGGACGACCTTAAGGCA 3584
Qy 4097 CAATGCCACACACACAGTGTCCGACACAGGCGGTGCGGTATGTTGTTGAA 4156
Db 3585 CAATGCCACACACACAGTGTCCGACACAGGCGGTGCGGTATGTTGTTGAA 3644
Qy 4157 ATGAGCTCGGAGATTGGGCTCGACCGCTGACGCAATGAGACTTTAAGCAGCGGACG 4216
Db 3645 ATGAGCTCGGAGATTGGGCTCGACCG-TGACGCAATGAGACTTTAAGCAGCGGACG 3703
Qy 4217 AAGAATATGAGGACGAGTGTGTTGTTATCTGATTAAGTCAAGGATTAATCCCGTTG 4276
Db 3704 AAGAATATGAGGACGAGTGTGTTGTTATCTGATTAAGTCAAGGATTAATCCCGTTG 3763
Qy 4277 CGGTGCTGTTAAGCGTGAAGGCGAGTGTGTTGTTATCTGATTAAGTCAAGGATTAATCCCGTTG 4336
Db 3764 CGGTGCTGTTAAGCGTGAAGGCGAGTGTGTTGTTATCTGATTAAGTCAAGGATTAATCCCGTTG 3823
Qy 4337 CCACACAGACATTAATAGCTGACAGACTTAACAGACTGTTCCATTCAGGCTTTTTCGCA 4396
Db 3824 CCACACAGACATTAATAGCTGACAGACTTAACAGACTGTTCCATTCAGGCTTTTTCGCA 3883
Qy 4397 GTCAACGTCACGCGT 4412
Db 3884 GTCAACGTCACGCGT 3899

RESULT 11
AB259286
ID AB259286 standard; DNA; 5500 BP.
XX
AC AB259286;
XX
DT 10-MAY-2003 (first entry)
XX
XX
DE Plasmid pPUV2002 SEQ ID NO 1.
XX
XX ADP-riboseylating exotoxin; immune response; immunisation; vaccine;
XX adjutant; cholera toxin subunit A; CTa; human cytomegalovirus; hCMV;
XX human tissue plasmidogen activator; circular; cyclic; ds.
XX
XX Synthetic.
XX
XX WO2003004055-A2.
XX
XX PD 16-JAN-2003.
XX
XX PF 26-NOV-2001; 2001MO-US043151.
XX
XX PR 27-NOV-2000; 2000US-00724315.
XX
XX PA (POWDER-) POWDERJECT VACCINES INC.

PI Haynes JR, Arrington JE;
XX WPI; 2003-221541/21.
XX
PT New compositions comprising nucleic acid adjuvants, useful in
PT immunization techniques, particularly for eliciting or enhancing an
PT immune response against an antigen in a human.
XX
XX Example 1; Fig 1; 143pp; English.
CC The invention relates to a composition comprising: (a) a first nucleic
CC acid sequence that is a truncated A subunit coding region obtained or
CC derived from a bacterial ADP-ribosylating exotoxin; and (b) a second
CC nucleic acid sequence that is a truncated B subunit coding region
CC obtained or derived from a bacterial ADP-ribosylating exotoxin. Each of
CC the truncated subunit coding regions has a 5' deletion and encodes a
CC subunit peptide not having an amino terminal bacterial signal peptide.
CC The composition is useful for eliciting an immune response against an
CC antigen or for manufacturing a medicament for enhancing an immune
CC response in a vertebrate subject (specifically a human) against an
CC antigen. The composition is particularly useful as nucleic acid adjuvants
CC for use in immunisation techniques. The present sequence is that of a
CC plasmid expression vector that contains a truncated coding sequence for a
CC cholera toxin (CT) subunit A (CTA) peptide, the human cytomegalovirus
CC (hCMV) immediate early promoter and associated intron A sequence and the
CC coding sequence for the signal peptide of human tissue plasminogen
CC activator, to allow for secretion from mammalian cells of the truncated
CC CTA expression product
XX
XX Sequence 5500 BP; 1373 A; 1336 C; 1373 G; 1418 T; 0 U; 0 Other;
SQ
Query Match 37.1%; Score 2378.8; DB 7; Length 5500;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 2598; Conservative 0; Mismatches 197; Indels 41; Gaps 6;

DB 1607 ATACTCAGCGGTGAGCATTTGAGAAACGCCACGCTTCCGAAAGGAGAAAGCGGACG 1666
QY 2215 GTATCCGGTAAGCGGAGGGGTGCGAACAGAGAGCGACAGAGGAGCTTCCAGGGGGAAA 2274
DB 1667 GTATCCGGTAAGCGGAGGGGTGCGAACAGAGAGCGACAGAGGAGCTTCCAGGGGGAAA 1726
QY 2275 CGCTGGATCTTTATAGTCTGTGCGGGTTTGCCACCTTGACTTGAAGCGTGAATTTT 2334
DB 1727 CGCTGGATCTTTATAGTCTGTGCGGGTTTGCCACCTTGAAGCGTGAATTTT 1786
QY 2335 GTGATCTCTGTCAGGGGGGGCGAGGCTATGAAAAACGCACAAACGCGGCTTTTACG 2394
DB 1787 GTGATCTCTGTCAGGGGGGGCGAGGCTATGAAAAACGCACAAACGCGGCTTTTACG 1846
QY 2395 GTTCCGAGCTTTTGTGCGGCTTTTGTGCACATGTTCTTCCGTGATTCCTCGATTC 2454
DB 1847 GTTCCGAGCTTTTGTGCGGCTTTTGTGCACATGTTCTTCCGTGATTCCTCGATTC 1906
QY 2455 TGTGATTAACCGATTAACCGGATGCGATGATTAATTAATTAATTC-----AATTA 2505
DB 1907 TGTGATTAACCGATTAACCGGATGCGATGATTAATTAATTAATTC-----AATTA 1966
QY 2506 CGGGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2565
DB 1967 CGAGCGCAAGAGTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2026
QY 2566 GCCCGCTGAGTCAAGCGGCGCAACGAGCGGCGCAATGAGTCAATTAATTAATTAATTA 2620
DB 2027 CCGCGCGCTGAGTCAAGCGGCGCAACGAGCGGCGCAATGAGTCAATTAATTAATTAATTA 2086
QY 2621 -----ATCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2657
DB 2087 GGGCAGTGAAGCGCAACGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2146
QY 2658 CCGATGAAGCGCAACGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2217
DB 2147 ACACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2206
QY 2718 AATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2777
DB 2207 AGGAAACAGCTATGACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2266
QY 2778 GGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2837
DB 2267 GGCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2326
QY 2838 TATGACCGGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2897
DB 2327 TATGACCGGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2386
QY 2898 CATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2957
DB 2387 CATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2446
QY 2958 CTGGCTGAAGCGGCGCAACGAGCGGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3017
DB 2447 CTGGCTGAAGCGGCGCAACGAGCGGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2505
QY 3018 TAAAGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3077
DB 2506 TAAAGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2565
QY 3078 ACTTGACAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3136
DB 2566 ACTTGACAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2625
QY 3137 GGTAAATGAGCGGCGCTGAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3196
DB 2626 GGTAAATGAGCGGCGCTGAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2685
QY 3197 CAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3256
DB 2686 CAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2745

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QY 3257 AATGGCGGTGATAGCGGTTTGACTCAACGGGGATTTCCAAAGTCTTCCACCCCATTTAGAGTC 3316
DB AATGGGGGTGATAGCGGTTTGACTCAACGGGGATTTCCAAAGTCTTCCACCCCATTTAGAGTC 2855
QY 3317 AATGGAGTTTGTTTTGGACCAAAATCAACGGGACTTTCCAAATGTCGTAATTAACCC 3376
DB AATGGAGTTTGTTTTGGACCAAAATCAACGGGACTTTCCAAATGTCGTAATTAACCC 2865
QY 3377 GCCCGTTGAACGAAATGGCGGTAGGCGGTGTACGGTGGAGGTCTATATTAAGCAGACT 3436
DB GCCCGTTGAACGAAATGGCGGTAGGCGGTGTACGGTGGAGGTCTATATTAAGCAGACT 2925
QY 3437 CGTTTATGAACCGTCAGATGCGCTGAGAGAGCCATCCAGCTGTTTGAAGCTTCAATAGA 3496
DB CGTTTATGAACCGTCAGATGCGCTGAGAGAGCCATCCAGCTGTTTGAAGCTTCAATAGA 2985
QY 3497 AGACACGGGGACCGATCCAGCTCCGCGGCGGGAGCGGTGCATTGGAAAGCGGATTCCTC 3556
DB AGACACGGGGACCGATCCAGCTCCGCGGCGGGAGCGGTGCATTGGAAAGCGGATTCCTC 3045
QY 3557 CGTCCAAAGATGACGTAAAGTACCGCTATAGACTATAGAGCAACCCCTTTGGCTCTT 3616
DB CGTCCAAAGATGACGTAAAGTACCGCTATAGACTATAGAGCAACCCCTTTGGCTCTT 3105
QY 3617 ATGCATGCTATCTGTTTGGCTTGGGCGCTTATACACCCCGCTTCTTATGCTATAGG 3676
DB ATGCATGCTATCTGTTTGGCTTGGGCGCTTATACACCCCGCTTCTTATGCTATAGG 3164
QY 3677 TGATGATATAGCTATAGCTATAGGTTGGGTATTTAGCACTATTTGAACCACTCCCTATT 3736
DB TGATGATATAGCTATAGCTATAGGTTGGGTATTTAGCACTATTTGAACCACTCCCTATT 3224
QY 3737 GGTACGATATCTTCCATTACTATCAATACATGAGCTTTGGCACAACATATCTATT 3796
DB GGTACGATATCTTCCATTACTATCAATACATGAGCTTTGGCACAACATATCTATT 3284
QY 3797 GGTATATGCAATATCTCTGTCTTCAAGAGCTGACACGAGCTCTGTATTTTAAAGAGT 3856
DB GGTATATGCAATATCTCTGTCTTCAAGAGCTGACACGAGCTCTGTATTTTAAAGAGT 3344
QY 3857 GGGGTCCTATTTATTTAATAATTCATATCAATCAACAGCGGTCGCCGTCGCGCA 3916
DB GGGGTCCTATTTATTTAATAATTCATATCAATCAACAGCGGTCGCCGTCGCGCA 3404
QY 3917 GTTTTATTTAATAAGTGGGATCTTCCACGCAATCTCGGTAACGTTCCGGAATG 3976
DB GTTTTATTTAATAAGTGGGATCTTCCACGCAATCTCGGTAACGTTCCGGAATG 3464
QY 3977 GGTCTTCTCGGTAGCGGCGGAGCTTCCATCCAGCCCTGTGTCCTGATCCCTCAAGC 4036
DB GGTCTTCTCGGTAGCGGCGGAGCTTCCATCCAGCCCTGTGTCCTGATCCCTCAAGC 3524
QY 4037 GCTCATGCTGCTGGGAGCTCTTGTCTTAAAGTGGAGCCAGACTTAAGGACAGCA 4096
DB GCTCATGCTGCTGGGAGCTCTTGTCTTAAAGTGGAGCCAGACTTAAGGACAGCA 3584
QY 4097 CAATGCCACACCAACAGTGTGCGCAACAAGCCGTGGAGGTATGTCTGAAA 4156
DB CAATGCCACACCAACAGTGTGCGCAACAAGCCGTGGAGGTATGTCTGAAA 3644
QY 4157 ATGAGCTCGAGATTTGGCTGCAACCGCTGACGAGATGAAAGATTAAAGGACGCGAG 4216
DB ATGAGCTCGAGATTTGGCTGCAACCGCTGACGAGATGAAAGATTAAAGGACGCGAG 3703
QY 4217 AAGAAGATGACGGAGCTGAGTTGTGTATCTGATAGAGCTAGAGGTAATCCCGTTG 4276
DB AAGAAGATGACGGAGCTGAGTTGTGTATCTGATAGAGCTAGAGGTAATCCCGTTG 3763
QY 4277 CGGTGCTGTTAACGCTGAGGCGAGTGTAGTCTGAGCAGTACTGTGCTGCTCGCGCGC 4336
DB CGGTGCTGTTAACGCTGAGGCGAGTGTAGTCTGAGCAGTACTGTGCTGCTCGCGCGC 3823

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QY 4337 CCACAGACATATAGCTGACAGACTAAGAGACTGTTCTTTCATGAGGCTTTTCTGCA 4396
DB 3824 CCACAGACATATAGCTGACAGACTAAGAGACTGTTCTTTCATGAGGCTTTTCTGCA 3883
QY 4397 GTCACCGTCCACGCGT 4412
DB 3884 GTCACCGTCCAGCTT 3899

RESULT 12
ADE06467
ID ADE06467 standard; DNA; 10466 BP.
XX
AC ADE06467;
XX
DT 29-JAN-2004 (first entry)
XX
DE Vector pGAL/IN2.
XX
KM HIV infection; Anti-HIV; vaccine; ds.
XX
OS Synthetic.
XX
FH Key
FT CDS
FT 99..1577
FT /product= "Gag, with inactivating point mutations in zinc
FT /finger packaging sequences for viral RNA"
FT CDS
FT 1382..3520
FT /tag= b
FT /product= "Pol, with inactivating point mutations in
FT reverse transcriptase, deletion of integrase"
FT exon
FT 3645..3859
FT /tag= c
FT /label= Tac_exon_#1
FT exon
FT 3784..3859
FT /tag= d
FT /label= Rev_exon_#1
FT CDS
FT 3873..4121
FT /tag= e
FT /product= "Vpu"
FT 4039..6642
FT /tag= f
FT /product= "Env"
FT 6205..6452
FT /tag= h
FT /label= Rev_exon_#2
FT exon
FT 6205..6295
FT /tag= g
FT /label= Tac_exon_#2

W02003076591-A2.
XX
PD 18-SEP-2003.
XX
PF 10-MAR-2003; 2003MO-US0071177.
XX
PR 08-MAR-2002; 2002US-00093953.
XX
PR 03-JAN-2003; 2003US-00336566.
XX
PA (UTEM-) UNIV EMORY.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI Robinson HL, Smith J, Hua J, Moss B;
XX
DR WPI; 2003-731822/69.
XX
PT A composition for generating an immune response against HIV comprises a
PT vector comprising a vaccine insert encoding one or more antigens that
PT elicit an immune response against HIV.
XX
PS Example 16; Fig 18; 133pp; English.
XX

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The present invention relates to a composition comprising a first vector with a vaccine insert encoding one or more antigens that elicit an immune response against HIV or a first subtype or recombinant form; and a second vector comprising a vaccine insert encoding one or more antigens that elicit an immune response against an HIV of a second subtype or recombinant form. The composition is useful in generating an immune response against HIV. The insert of the first vector or the insert of the second vector comprises the sequences of two or more of: a gag, pol, env, tat, rev, nef, vif, vpr or vpu gene; or their mutants; and optionally, non-coding regulatory sequences of the HIV genome. At least one of the two or more sequences comprises mutations that limit the encapsidation of viral RNA, or a gag sequence having a mutation in one or more of the sequences encoding a zinc finger. All or part of cis-acting RNA encapsidation sequences have been deleted from the non-coding regulatory sequences of HIV-1. The two or more sequences comprise a pol sequence having a mutation that inhibits one or more of the enzymatic activities of pol. The enzymatic activity is integrase activity, reverse transcriptase activity or protease activity. The enzymatic activity is inhibited by deleting a portion of the pol sequence or introducing one or more point mutations into the pol sequence. The present sequence is one such vector used to illustrate the invention.

SQ Sequence 10466 BP; 3317 A; 2200 C; 2543 G; 2405 T; 0 U; 1 Other;

Query Match	31.6%	Score 2027.6;	DB 9;	Length 10466;
Best Local Similarity	87.4%	Pred. No. 0;		
Matches 2407;	Conservative	1;	Mismatches 15;	Indels 331; Gaps 4;

QY	1654	ACCTCATTTTAAATTAAAGATCTAGGTGAAGATCCTTTTGTATATCTCATGACCA	1713
Db	8041	ACTGGCTTCTACGTAAAGGATCTAGGTGAAGATCCTTTTGTAAATCTCATGACCA	8100
QY	1714	AATCCCTTAAGGTAGTTCCTTTCCTTCACAGACGTCAGACCCCGTAGAAAAAGATCAAGG	1773
Db	8101	AATCCCTTAAGGTAGTTCCTTTCCTTCACAGACGTCAGACCCCGTAGAAAAAGATCAAGG	8160
QY	1774	ATCTTCTTGAGATCCTTTTTCCTGGCGGTAACTGCTGCTTGCAAAAGAAAAACCAAC	1833
Db	8161	ATCTTCTTGAGATCCTTTTTCCTGGCGGTAACTGCTGCTTGCAAAAGAAAAACCAAC	8220
QY	1834	GCTACACAGGGGTGTTTGTTCGCCGATCAAGAGCTACCAACTCTTTTCCGAAGGTAC	1893
Db	8221	GCTACACAGGGGTGTTTGTTCGCCGATCAAGAGCTACCAACTCTTTTCCGAAGGTAC	8280
QY	1894	TGGCTTACAGACGCGCAGATACCAATACTGTTCTTCTAGTGACCGGTAGTGAAGCCA	1953
Db	8281	TGGCTTACAGACGCGCAGATACCAATACTGTTCTTCTAGTGACCGGTAGTGAAGCCA	8340
QY	1954	CCACTTCAAGAACTCTGTAGACACGGCGCTACATACCTCGCTGCTATACCTGTATCCAGT	2013
Db	8341	CCACTTCAAGAACTCTGTAGACACGGCGCTACATACCTCGCTGCTATACCTGTATCCAGT	8400
QY	2014	GCGTCTGCGCACTGCGCATTAAGTCGTGCTTTACCGGGTTTGACCTCAGACGATAGTTAC	2073
Db	8401	GCGTCTGCGCACTGCGCATTAAGTCGTGCTTTACCGGGTTTGACCTCAGACGATAGTTAC	8460
QY	2074	GGATTAAGGCGCGACCGCTGCGGTGTAACGGGGGGTTCGTGCACACAGCCCACTTTGAGCG	2133
Db	8461	GGATTAAGGCGCGACCGCTGCGGTGTAACGGGGGGTTCGTGCACACAGCCCACTTTGAGCG	8520
QY	2134	AACGACCTACACCGAAGTGAATACCTACAGCGTACGATATGAGAAACGCGCACCTTCC	2193
Db	8521	AACGACCTACACCGAAGTGAATACCTACAGCGTACGATATGAGAAACGCGCACCTTCC	8580
QY	2194	CGAAGGAGAAAGCGCGGACAGGTATCCGCTAAAGCGCAGGGTCGAAACAGAGAGCGAC	2253
Db	8581	CGAAGGAGAAAGCGCGGACAGGTATCCGCTAAAGCGCAGGGTCGAAACAGAGAGCGAC	8640
QY	2254	GAGGAGGCTTCCAGGGGGGAAAACGCTGGATCTTTATATGCTCTGTCGGGTTTCGCACT	2313
Db	8641	GAGGAGGCTTCCAGGGGGGAAAACGCTGGATCTTTATATGCTCTGTCGGGTTTCGCACT	8700
QY	2314	CTGACTTGAGCGTCGATTTTGTGATGCTCTGTCAGGGGGGCGAGCCATATGAAAAAGC	2373

Dd	8701	CTGACTGAGCGTGCATTTTGTGATCTGTCAGGGGGGGGAGCCTTAGGAAAAAGC	8760
Qy	2374	CAGCAACGCGGCTTTTTCACGGTTCCTGGCCTTTTGTGCGCTTTTCTCACATGTTCTT	2433
Dd	8761	CAGCAACGCGGCTTTTTCACGGTTCCTGGCCTTTTGTGCGCTTTTCTCACATGTTGT-	8819
Qy	2434	TCCTGCGTTATCCCTGATTCGTGGATTAACCGTATTACGCCCATGATTAAGTTATTAAT	2493
Dd	8820	-----	8819
Qy	2494	AGTATGCAATTACGGGGGTCATTAGTGTATAGGCCATPATAGAGTTCCGGTTACATTAAC	2553
Dd	8820	-----	8819
Qy	2554	TTACGGTAAATAGCCCGCTGGCTGACCGCCCAACGACCCCGCCCATTTGACGTCAATAA	2613
Dd	8820	-----	8819
Qy	2614	TGACGAGATCTGATATAGTGTCAGACGATATGAGGCTATATCGCCGATAGAGCGCAT	2673
Dd	8820	-----	8819
Qy	2674	CAAGCTGCAACATGGCCAAATGCATATGCATCTATACATTTGAATCAATATTGGCAATTAGC	2733
Dd	8820	-----	8819
Qy	2734	CATATAGTCAATGGTTATATATAGCATAAATCAATATTGGCTATTGGCATTTGCATACGTT	2793
Dd	8820	-----CGACAAATTTGGCATTTGGCATTTGGCATTTGCATACGTT	8852
Qy	2794	GTATCTATATCAATATATATGATACATTATATTTGGTCTCATGTCCAATATGACCGCATGTTG	2853
Dd	8853	GTATCTATATCAATATATATGATACATTATATTTGGTCTCATGTCCAATATGACCGCATGTTG	8912
Qy	2854	ACATTGATATTGTAAGTACTGATTTAATAGTAATCAATACGGGGCTTAGTGTCAATAGCCC	2913
Dd	8913	ACATTGATATTGTAAGTACTGATTTAATAGTAATCAATACGGGGCTTAGTGTCAATAGCCC	8972
Qy	2914	ATATATGAGATTCGCGGTTACATTAACCTTAACGGTAAATGAGCCGCGCTGGCTGACCGCCAA	2973
Dd	8973	ATATATGAGATTCGCGGTTACATTAACCTTAACGGTAAATGAGCCGCGCTGGCTGACCGCCAA	9032
Qy	2974	CGACCCCGCCCATTTGACGTCAATGATGACGTATGTTCCCATAGTAAAGCCCAATAGGAGAC	3033
Dd	9033	CGACCCCGCCCATTTGACGTCAATGATGACGTATGTTCCCATAGTAAAGCCCAATAGGAGAC	9092
Qy	3034	TTTTCATTGACGTCAATGGGTGGAGTATTTACGGTAAATGCCCCCATTTGGCAGTACATCA	3093
Dd	9093	TTTTCATTGACGTCAATGGGTGGAGTATTTACGGTAAATGCCCCCATTTGGCAGTACATCA	9152
Qy	3094	AGTGATCATATGCAAGTCCGCCCCCATTTGACGTCAATGACGGTAAATGAGCCGCGCTG	3153
Dd	9153	AGTGATCATATGCAAGTCCGCCCCCATTTGACGTCAATGACGGTAAATGAGCCGCGCTG	9212
Qy	3154	GCATTATGCCAGTACATGACCTTATACGGGACTTTCTTACTTGGAGTACATCTAC-GTAT	3212
Dd	9213	GCATTATGCCAGTACATGACCTTATACGGGACTTTCTTACTTGGAGTACATCTACGCTAT	9272
Qy	3213	TAGTCATTC-GTATATTAACATGGGTATCGGTTTGGCAGTACACCAATGGGCGTGATAG	3271
Dd	9273	TAGTCATTCGGCTATTAACATGGGTATCGGTTTGGCAGTACACCAATGGGCGTGATAG	9332
Qy	3272	CGGTTTGAATCAGCGGGGATTTTCAAGTCTCAACCCCATTTGACGTCAATGGGAGTTGTT	3331
Dd	9333	CGGTTTGAATCAGCGGGGATTTTCAAGTCTCAACCCCATTTGACGTCAATGGGAGTTGTT	9392
Qy	3332	TGGCAACCAAAATCAACGGGACTTTTCAAAATGTGTATATAACCCCGCCGCTTGACGCAA	3391
Dd	9393	TGGCAACCAAAATCAACGGGACTTTTCAAAATGTGTATATAACCCCGCCGCTTGACGCAA	9452
Qy	3392	ATGGCGGTAGCGCGTGTACGGTGGAGGCTTATATTAAGCAGAGCTTCGTTTAGTAAACCGT	3451


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Db      9453 ATGGGCGGTAGGCGGTGATCGGTGGAGGTCTATATAGACAGAGCTGTTTAGTAACCGT 9512
QY      3452 CAGATCCCTGAGAGACCCATCCAGCTGTTTGACTCCATAGAGACACCCGGACCGA 3511
Db      9513 CAGATCCCTGAGAGACCCATCCAGCTGTTTGACTCCATAGAGACACCCGGACCGA 9572
QY      3512 TCCAGCTCCGCGCGCGGGAACGGTGAATTGGAAACGGGGAATCCCGCGCAAGAGAC 3571
Db      9573 TCCAGCTCCGCGCGCGGGAACGGTGAATTGGAAACGGGGAATCCCGCGCAAGAGAC 9632
QY      3572 GTAAGTACCGCTATAGACTCTATAGGACACCCCTTGGCTCTTATGCAATGCTATAGT 3631
Db      9633 GTAAGTACCGCTATAGACTCTATAGGACACCCCTTGGCTCTTATGCAATGCTATAGT 9692
QY      3632 TTTTGGCTTGGGCGCTATACACCCCGCTTCTTATGCTATAGTATAGTATAGCTTA 3691
Db      9693 TTTTGGCTTGGGCGCTATACACCCCGCTTCTTATGCTATAGTATAGTATAGCTTA 9752
QY      3692 GCCATAGGTGGGTATATGACATATATGACACACCTCCCTATGCTGACATATCTTC 3751
Db      9753 GCCATAGGTGGGTATATGACATATATGACACACCTCCCTATGCTGACATATCTTC 9812
QY      3752 CATTACTAATCATATACATGCTCTTGGCCACAACATATCTTATGCTATATGCTATAT 3811
Db      9813 CATTACTAATCATATACATGCTCTTGGCCACAACATATCTTATGCTATATGCTATAT 9872
QY      3812 CTCTGCTCTTCAAGACTGACACGAGCTGTATATTTTAAAGATGGGGTCCATTTATT 3871
Db      9873 CTCTGCTCTTCAAGACTGACACGAGCTGTATATTTTAAAGATGGGGTCCATTTATT 9932
QY      3872 ATTTCACAATTCATATACAAACACCGCCGCGCCGCGGAGTTTATTTATTAACAT 3931
Db      9933 ATTTCACAATTCATATACAAACACCGCCGCGCGGAGTTTATTTATTTAAACAT 9992
QY      3932 AGCGTGGGATCTCCACCGCAATCTCGGGTA-CGTGTCCGGAATGGGCTCTTCTCCGCT 3990
Db      9993 AGCGTGGGATCTCCACCGCAATCTCGGGTACCGGTCTCCGGAATGGGCTCTTCTCCGCT 10052
QY      3991 AGCGGCGGAGCTTCCACATCCGAGCCCTGTCCCATGCTCCAGCGGCTCATGGTCTC 4050
Db      10053 AGCGGCGGAGCTTCCACATCCGAGCCCTGTCCCATGCTCCAGCGGCTCATGGTCTC 10112
QY      4051 GGCAGCTCTTGTCTCTTAACGTGAGGCCAGACTTATAGGACACAGCAATGCCACCA 4110
Db      10113 GGCAGCTCTTGTCTCTTAACGTGAGGCCAGACTTATAGGACACAGCAATGCCACCA 10172
QY      4111 ACCAGTGTCCGCAACAGGCCGTGGGTAGGGTATGCTGAATATGAGCTCGAGAT 4170
Db      10173 ACCAGTGTCCGCAACAGGCCGTGGGTAGGGTATGCTGAATATGAGCTCGAGAT 10232
QY      4171 TGGGCTGCAACCGCTGACGAGATGAGAACTTAAAGCAGCGGACGAGAAAGATGACGC 4230
Db      10233 TGGGCTGCAACCGCTGACGAGATGAGAACTTAAAGCAGCGGACGAGAAAGATGACGC 10292
QY      4231 AGCTGAGTTGTTGATTTCTGATTAAGTCAAGGTAATCTCCGTTGGGCTGTTAACG 4290
Db      10293 AGCTGAGTTGTTGATTTCTGATTAAGTCAAGGTAATCTCCGTTGGGCTGTTAACG 10352
QY      4291 GTGAGGGGAGTGAAGTCTGAGCAGTACTGTTCTCGCGCGGCGGACACAGCATAT 4350
Db      10353 GTGAGGGGAGTGAAGTCTGAGCAGTACTGTTCTCGCGCGGCGGACACAGCATAT 10412
QY      4351 AGCTGACAGTAAACAGCTGTTCTTTTCAATGGGCTCTTTCTGCACTCAACCGT 4404
Db      10413 AGCTGACAGTAAACAGCTGTTCTTTTCAATGGGCTCTTTCTGCACTCAACCGT 10466

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DT      29-JAN-2004 (first entry)
XX      DE      Vector pGAL/IN3.
XX      KM      HIV Infection; Anti-HIV; vaccine; ds.
XX      OS      Synthetic.
XX      PH      Key
XX      FT      CDS
XX      FT      Location/Qualifiers
XX      FT      99..1577
XX      FT      /*tag= a
XX      FT      /product= "Gag, with inactivating point mutations in zinc
XX      FT      finger packaging sequences for viral RNA"
XX      FT      1382..3520
XX      FT      CDS
XX      FT      /*tag= b
XX      FT      /product= "Pol, with inactivating point mutations in
XX      FT      reverse transcriptase, deletion of integrase"
XX      FT      3645..3859
XX      FT      exon
XX      FT      /*tag= c
XX      FT      /label= Tat_exon_#1
XX      FT      3784..3859
XX      FT      exon
XX      FT      /*tag= d
XX      FT      /label= Rev_exon_#1
XX      FT      3873..4121
XX      FT      CDS
XX      FT      /*tag= e
XX      FT      /product= "Vpu"
XX      FT      4039..6642
XX      FT      /*tag= f
XX      FT      /product= "Env"
XX      FT      6205..6452
XX      FT      exon
XX      FT      /*tag= h
XX      FT      /label= Rev_exon_#2
XX      FT      6205..6295
XX      FT      exon
XX      FT      /*tag= g
XX      FT      /label= Tat_exon_#2
XX      PN      MO2003076591-A2.
XX      PD      18-SEP-2003.
XX      PF      10-MAR-2003; 2003MO-US007177.
XX      PR      08-MAR-2002; 2002US-00093953.
XX      PR      03-JAN-2003; 2003US-00336566.
XX      PA      (UYEM-) UNIV EMORY.
XX      PA      (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX      PI      Robinson HL, Smith J, Hua J, Moss B;
XX      DR      WPI; 2003-731822/69.
XX      PT      A composition for generating an immune response against HIV comprises a
XX      PT      vector comprising a vaccine insert encoding one or more antigens that
XX      PT      elicit an immune response against HIV.
XX      PS      Example 15; Fig 17; 133pp; English.
XX
XX      The present invention relates to a composition comprising a first vector
XX      with a vaccine insert encoding one or more antigens that elicit an immune
XX      response against HIV or a first subtype or recombinant form; and a second
XX      vector comprising a vaccine insert encoding one or more antigens that
XX      elicit an immune response against an HIV of a second subtype or
XX      recombinant form. The composition is useful in generating an immune
XX      response against HIV. The insert of the first vector or the insert of the
XX      second vector comprises the sequences of two or more of: a gag, pol, env,
XX      tat, rev, nef, vif, vpr or vpu gene; or their mutants, and optionally;
XX      non-coding regulatory sequences of the HIV genome. At least one of the
XX      two or more sequences comprises mutations that limit the encapsidation of
XX      viral RNA, or a gag sequence having a mutation in one or more of the
XX      sequences encoding a zinc finger. All or part of cis-acting RNA
XX      encapsidation sequences have been deleted from the non-coding regulatory
XX      sequences of HIV-1. The two or more sequences comprise a pol sequence

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CC having a mutation that inhibits one or more of the enzymatic activities
of pol. The enzymatic activity is integrase activity, reverse
transcriptase activity or protease activity. The enzymatic activity is
inhibited by deleting a portion of the pol sequence or introducing one or
more point mutations into the pol sequence. The present sequence is one
such vector used to illustrate the invention.

XX Sequence 10466 BP; 3316 A; 2205 C; 2539 G; 2405 T; 0 U; 1 Other;

Query Match 31.6%; Score 2027.6; DB 9; Length 10466;

Best Local Similarity 87.4%; Pred. No. 0;

Matches 2407; Conservative 1; Mismatches 15; Indels 331; Gaps 4;

Qy	1654	ACTTCAATTTTAAATTTAAAGATCTAGTGAAGATCTTTTGTATATCTCATGACCA	1713
Db	8041	ACTGCGTTTCTACGTGAAAAGATCTAGTGAAGATCTTTTGTATATCTCATGACCA	8100
Qy	1714	AATCCCTTAACGTAGTTCGTTCCACTGAGGCTCAGACCCCGTAGAAAAGTCAAAG	1773
Db	8101	AATCCCTTAACGTAGTTCGTTCCACTGAGGCTCAGACCCCGTAGAAAAGTCAAAG	8160
Qy	1774	ATCTCTTGAGATCTTTTTCGCGCGATCTGCTGCTGCAACAAAACCAACACC	1833
Db	8161	ATCTCTTGAGATCTTTTTCGCGCGATCTGCTGCTGCAACAAAACCAACACC	8220
Qy	1834	GCTACACGCGGTGTTTGTTCGCGATCAAGACTACCACTCTTTTCCGAAAGTAA	1893
Db	8221	GCTACACGCGGTGTTTGTTCGCGATCAAGACTACCACTCTTTTCCGAAAGTAA	8280
Qy	1894	TGCTCTCAGACAGCGGATACCAATCTGTTCTTCTAGTACCGCTTAGTACCA	1953
Db	8281	TGCTCTCAGACAGCGGATACCAATCTGTTCTTCTAGTACCGCTTAGTACCA	8340
Qy	1954	CCACTTCAAGAACTCTGTACACCGCTCATACCTGCTCTGTAATCTGTTACAGT	2013
Db	8341	CCACTTCAAGAACTCTGTACACCGCTCATACCTGCTCTGTAATCTGTTACAGT	8400
Qy	2014	GCTGCTGCGAGTGGGATAGTCTGTCTTACCGGCTTGAATCAAGACGATAGTAC	2073
Db	8401	GCTGCTGCGAGTGGGATAGTCTGTCTTACCGGCTTGAATCAAGACGATAGTAC	8460
Qy	2074	GATTAAGCGGACGCGTGGGCTGAAAGGGGGGTTGTGCAACAGCCGCTTGAGG	2133
Db	8461	GATTAAGCGGACGCGTGGGCTGAAAGGGGGGTTGTGCAACAGCCGCTTGAGG	8520
Qy	2134	AACGACTACACCGAACTGAGATACCTACGCGGTAGCTATGAAAAGGCGCAGCTTC	2193
Db	8521	AACGACTACACCGAACTGAGATACCTACGCGGTAGCTATGAAAAGGCGCAGCTTC	8580
Qy	2194	CGAAGGGAAGAAAGCGGACAGTATCCGTTAGCGGAGGCTCGAAACAGAGAGCGAC	2253
Db	8581	CGAAGGGAAGAAAGCGGACAGTATCCGTTAGCGGAGGCTCGAAACAGAGAGCGAC	8640
Qy	2254	GAGGAGCTTCGAGGGGAAAAGCGCTGTATCTTTATATGCTGTGGGTTTGCCACT	2313
Db	8641	GAGGAGCTTCGAGGGGAAAAGCGCTGTATCTTTATATGCTGTGGGTTTGCCACT	8700
Qy	2314	CTGACTTGAGCGTGAATTTTGTATGCTGTGACGGGGGGGAGAGCTATGAAAAGCG	2373
Db	8701	CTGACTTGAGCGTGAATTTTGTATGCTGTGACGGGGGGGAGAGCTATGAAAAGCG	8760
Qy	2374	CAGCAACGCGGCTTTTTCGTTTCTGCTGCTTGTGCTTTTGTCTCAATGTTCTT	2433
Db	8761	CAGCAACGCGGCTTTTTCGTTTCTGCTGCTTGTGCTTTTGTCTCAATGTTCTT	8819
Qy	2434	TCTGCGTTATCCCCTGATTTCTGTGATTAACCGTATTACCGCATGATTATTAAT	2493
Db	8820	-----	8819
Qy	2494	AGTATCATATTACGGGCTATTAGTTGATAGCCCATATGAGTTCCGGTTACATTAAC	2553
Db	8820	-----	8819

Qy	2554	TTACGGTAATGCGCCGCTGGCTGACCGCCACGACGCCGCCCATTTGACGTCAATTA	2613
Db	8820	-----	8819
Qy	2614	TGACGAGATCTGATATAGTGAACAGATATGAGGCTATATCGCGATGAGGGGACAT	2673
Db	8820	-----	8819
Qy	2674	CAAGCTGCACATGCGCAATGATATGATCTATACATTTGATATGCAATTGCAATTAGC	2733
Db	8820	-----	8819
Qy	2734	CATATTAGTCAATTGTTATATAGCAATTAATGCTATTTGGCTATTGGCCATTGCAATCGTT	2793
Db	8820	-----	8819
Qy	2794	GTAATCATTAATATATGATATTTATTTGGCTCATAGTCCAAATATGACCGGCTG	2853
Db	8853	GTAATCATTAATATATGATATTTATTTGGCTCATAGTCCAAATATGACCGGCTG	8912
Qy	2854	ACATTGATTTGACTAGTTATTAATAGTAATCAATTAAGGGGCTATTAGTATAGGCC	2913
Db	8913	ACATTGATTTGACTAGTTATTAATAGTAATCAATTAAGGGGCTATTAGTATAGGCC	8972
Qy	2914	ATATATGAGTTCCGCTTACATTAACGTTAATGAGCCCGCTGCTGACCGCCAA	2973
Db	8973	ATATATGAGTTCCGCTTACATTAACGTTAATGAGCCCGCTGCTGACCGCCAA	9032
Qy	2974	CGACCCCGGCGATGAGTCAATGATGACGATGTCATGATGATGAGGCGCAATAGGAGC	3033
Db	9033	CGACCCCGGCGATGAGTCAATGATGACGATGTCATGATGATGAGGCGCAATAGGAGC	9092
Qy	3034	TTTCCATTGACGTCAATGGGAGTATTTACGTTAACTGGCCCACTTGGCAGTACATCA	3093
Db	9093	TTTCCATTGACGTCAATGGGAGTATTTACGTTAACTGGCCCACTTGGCAGTACATCA	9152
Qy	3094	AGTATATCATATGCAAGTCCGCTTATTTAGCTCAATGACGTTAAATGAGCCGCTG	3153
Db	9153	AGTATATCATATGCAAGTCCGCTTATTTAGCTCAATGACGTTAAATGAGCCGCTG	9212
Qy	3154	GGATTATGCGGACATGACCTTACCGGACCTTCTCTTGGCAGTACATGAC-GTAT	3212
Db	9213	GGATTATGCGGACATGACCTTACCGGACCTTCTCTTGGCAGTACATGAC-GTAT	9272
Qy	3213	TAGTCATC-GCTATTATCAATGATGAGCGTTTGGCAGTACACCAATGGGCTGATAG	3271
Db	9273	TAGTCATGCGCTATTATCAATGATGAGCGTTTGGCAGTACACCAATGGGCTGATAG	9332
Qy	3272	CGGTTGACTACGCGGGAATTTCAAGTCTCACCCCATTTGACGTCAATGGAGTTGTTT	3331
Db	9333	CGGTTGACTACGCGGGAATTTCAAGTCTCACCCCATTTGACGTCAATGGAGTTGTTT	9392
Qy	3332	TGGACCAAAATCAACGGGACCTTTCCAAATATGCTGTAATAACCCCGCGGTGACGCA	3391
Db	9393	TGGACCAAAATCAACGGGACCTTTCCAAATATGCTGTAATAACCCCGCGGTGACGCA	9452
Qy	3392	ATGGGCGATGAGGCTGATCGGTGGAGGCTATATTAAGACAGAGCTGTTAGTGAACGCT	3451
Db	9453	ATGGGCGATGAGGCTGATCGGTGGAGGCTATATTAAGACAGAGCTGTTAGTGAACGCT	9512
Qy	3452	CAGATGCTGAGAGCGCCATCAACGCTGTTTGAACCTTCATTAAGAAAGACCGGAGCGCA	3511
Db	9513	CAGATGCTGAGAGCGCCATCAACGCTGTTTGAACCTTCATTAAGAAAGACCGGAGCGCA	9572
Qy	3512	TCCAGCTCCGGGCGGGAAGCGGCAATTTGAAGCGGCAATCCCGTGGCAAGAGTGA	3571
Db	9573	TCCAGCTCCGGGCGGGAAGCGGCAATTTGAAGCGGCAATCCCGTGGCAAGAGTGA	9632
Qy	3572	GTAATGACCGCTATGACTCTATAGGACACCCCTTTGGCTCTTAATGATCTATACG	3631
Db	9633	GTAATGACCGCTATGACTCTATAGGACACCCCTTTGGCTCTTAATGATCTATACG	9692
Qy	3632	TTTTGGCTTGGGCGCTATACACCCCGCTTCTATAGTATAGTATAGCTTAA	3691

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Db      9693 TTTTGGCTTGGGGCCCTATACACCCCGCTTCCCTTAAGCTATAGTATAGTATAGCTTA
          |||
Qy      3692 GCGTAAGTGTGTGGTATTGACATTATGACACCTCCCTATTGGTGAAGATATCTTC
          |||
Db      9753 GCGTAAGTGTGTGGTATTGACATTATGACACCTCCCTATTGGTGAAGATATCTTC
          |||
Qy      3752 CATTACTAATCCATTAATAGTCTTTGGCCAACTATCTCTATTTGGCTATATGCCAATA
          |||
Db      9813 CATTACTAATCCATTAATAGTCTTTGGCCAACTATCTCTATTTGGCTATATGCCAATA
          |||
Qy      3812 CTCTGTCTTCAGAGACTGACAGGACTCTGTATTTTAAAGATGGGGTCCCATTTAT
          |||
Db      9873 CTCTGTCTTCAGAGACTGACAGGACTCTGTATTTTAAAGATGGGGTCCCATTTAT
          |||
Qy      3872 ATTACAAATTCATATACAAACACCGCTCCCGCGACGAGTTTATTTAAACAT
          |||
Db      9933 ATTACAAATTCATATACAAACACCGCTCCCGCGACGAGTTTATTTAAACAT
          |||
Qy      3932 AGGCTGGGATCTCAGCGGAATCTCGGGA-CTGTTCGCGACATGGGCTTCTCGGT
          |||
Db      9993 AGGCTGGGATCTCAGCGGAATCTCGGGA-CTGTTCGCGACATGGGCTTCTCGGT
          |||
Qy      3991 AGCGCGGAGCTTCCATCCGAGCCCTGTGCTCCATGCTCCAGCGGCTCATGGTGC
          |||
Db      10053 AGCGCGGAGCTTCCATCCGAGCCCTGTGCTCCATGCTCCAGCGGCTCATGGTGC
          |||
Qy      4051 GCGAGCTCTTGTCTCTTAAAGTGAAGGCGCACTTATAGGCAACATGCCACACC
          |||
Db      10113 GCGAGCTCTTGTCTCTTAAAGTGAAGGCGCACTTATAGGCAACATGCCACACC
          |||
Qy      4111 ACCAGTGTGCGGCAAGGCGGCTGTGGGTAATGTGTCTGAATATGAGCTCGAGAT
          |||
Db      10173 ACCAGTGTGCGGCAAGGCGGCTGTGGGTAATGTGTCTGAATATGAGCTCGAGAT
          |||
Qy      4171 TGGGCTGTGCAACCGGTGACGAGATGGAAGCTTAAAGGAGGAGAGAAAGATGCAAGC
          |||
Db      10233 TGGGCTGTGCAACCGGTGACGAGATGGAAGCTTAAAGGAGGAGAGAAAGATGCAAGC
          |||
Qy      4231 AGCTGAGTGTGTATCTGATTAAGATGACAGGTAATCTCCGTTGCGGTCTTTAACG
          |||
Db      10293 AGCTGAGTGTGTATCTGATTAAGATGACAGGTAATCTCCGTTGCGGTCTTTAACG
          |||
Qy      4291 GTGGAGGCGAGTGTGTCTGAGCAGTACTGTTCTCCGCGCGCCACCAACATAT
          |||
Db      10353 GTGGAGGCGAGTGTGTCTGAGCAGTACTGTTCTCCGCGCGCCACCAACATAT
          |||
Qy      4351 AGCTGAGAGCTAAGAGCTGTCTTCCATGAGGCTTTTCTGCACTCAACCGT
          |||
Db      10413 AGCTGAGAGCTAAGAGAGCTGTCTTCCATGAGGCTTTTCTGCACTCAACCAT
          |||

RESULT 14
ADE06463 standard; DNA, 10447 BP.
XX
AC ADE06463;
XX
DT 29-JAN-2004 (first entry)
XX
DE Vector pGAL/IC2.
XX
KW HIV infection; Anti-HIV; vaccine; ds.
XX
OS Synthetic.
XX
FH Key
FT CDS 104..1591
FT     /tag= a
FT     /product= "Gag, with inactivating point mutations in zinc
FT     finger packaging sequences for viral RNA"
FT CDS 1393..3576
FT     /**tag= b

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FT      /product= "Pol, with inactivating point mutations in
FT      reverse transcriptase, deletion of integrase"
FT      3693..3877
FT      /**tag= c
FT      /label= Tat_exon_#1
FT      3802..3877
FT      /**tag= d
FT      /label= Rev_exon_#1
FT      3904..4149
FT      /**tag= e
FT      /product= "Vpu"
FT      4067..4628
FT      /**tag= f
FT      /product= "Env"
FT      6215..6510
FT      /**tag= h
FT      /label= Rev_exon_#2
FT      6215..6305
FT      /**tag= g
FT      /label= Tat_exon_#2

PD      MO2003076591-A2.
PN      18-SEP-2003.
PF      10-MAR-2003; 2003MO-US007177.
PX      08-MAR-2002; 2002US-00093953.
PR      03-JAN-2003; 2003US-00336566.
PS      (UYEM-) UNIV EMORY
PA      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI      Robinson HL, Smith J, Hua J, Moss B;
XX      WPI; 2003-731822/69.
DR      A composition for generating an immune response against HIV comprises a
PT      vector comprising a vaccine insert encoding one or more antigens that
PT      elicit an immune response against HIV.
XX
XX      Example 12, Fig 14, 133pp; English:
XX
XX      The present invention relates to a composition comprising a first vector
XX      with a vaccine insert encoding one or more antigens that elicit an immune
XX      response against HIV or a first subtype or recombinant form; and a second
XX      vector comprising a vaccine insert encoding one or more antigens that
XX      elicit an immune response against an HIV of a second subtype or
XX      recombinant form. The insert of the first vector or the insert of the
XX      second vector comprises the sequences of two or more of: a gag, pol, env,
XX      tat, rev, nef, vif, vpr or vpu gene; or their mutants, and optionally;
XX      non-coding regulatory sequences of the HIV genome. At least one of the
XX      two or more sequences comprises mutations that limit the encapsidation of
XX      viral RNA, or a gag sequence having a mutation in one or more of the
XX      sequences encoding a zinc finger. All or part of cis-acting RNA
XX      encapsidation sequences have been deleted from the non-coding regulatory
XX      sequences of HIV-1. The two or more sequences comprise a pol sequence
XX      having a mutation that inhibits one or more of the enzymatic activities
XX      of pol. The enzymatic activity is integrase activity, reverse
XX      transcriptase activity or protease activity. The enzymatic activity is
XX      inhibited by deleting a portion of the pol sequence or introducing one or
XX      more point mutations into the pol sequence. The present sequence is one
XX      such vector used to illustrate the invention.
XX
SQ      Sequence 10447 BP; 3304 A; 2213 C; 2548 G; 2381 T; 0 U; 1 Other;
XX
Query Match 31.6%; Score 2027.2; DB 9; Length 10447;
Best Local Similarity 87.4%; Pred. No. 0;
Matches 2406; Conservative 1; Mismatches 14; Indels 331; Gaps 4;
Qy      1654 ACTTCATTTTAAATTAAGATCTAGGAGATCTTTGATATCTCATGACCA 1713
          |||

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Db 8024 ACTGCTTTCTACGTGAAAAAGATCTAGGTGAAGATCTTTTTGATGATCTCATGCAAA 8083
QY 1714 AATCCCTTAACGAGTTTTGTTTCAGTGAAGGTCAGAACCCCGTAGAAAAAGATCAAGG 1773
Db 8084 AATCCCTTAACGAGTTTTGTTTCAGTGAAGGTCAGAACCCCGTAGAAAAAGATCAAGG 8143
QY 1774 ATCTTCTGAGATCTTTTTTCTGCGCGTAACTCTGCTGTTGCAAAACAAAAACACCC 1833
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Dd		9976	AGCGTGGAATCTCACGCCAATCTCGGGTA - CGTGTTCGGCAATGGACTCTTTCGCGT	10035
Oy		3991	AGCGCGCAGATTCCAATCCGAGCCTTGCTCCCATGCTCCAGCGGCTCATGCTGCTC	4050
Dd		10036	AGCGCGCAGATTCCAATCCGAGCCTTGCTCCCATGCTCCAGCGGCTCATGCTGCTC	10095
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Dd		10096	GCGAGCTCCTTGTCTCTTAACAGTGGAGGCCAGA CTTAAGGACAGCA CAATGCCACACC	10155
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Dd		10156	ACCA GTGTGCGCACAAGCCGTGCGGTAGGGTAGTGCTGAAAATAAGCTCGAGAT	10215
Oy		4171	TGGCGTCGCACCGCTGACGCAATGGA GA CTTAAGGACGCGCAGAAGATGCA GCG	4230
Dd		10216	TGGCGTCGCACCGCTGACGCAATGGA GA CTTAAGGACGCGCAGAAGATGCA GCG	10275
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Dd		10276	AGCTGAGTTGTGTGATTTCTGATTAAGATCAAGATTA CTCCCCTGCTGCTTTAAAG	10335
Oy		4291	GTGAGGGCAGATGAGTCTGAGCAGTACTGTTGCTGCGCGCGGCCACAAGACATAAT	4350
Dd		10336	GTGAGGGCAGATGAGTCTGAGCAGTACTGTTGCTGCGCGCGGCCACAAGACATAAT	10395
Oy		4351	AGCTGACAGACTTAACAGACTGTTCTTTCCATGGGTCTTTTTCGACGTACC	4402
Dd		10396	AGCTGACAGACTTAACAGACTGTTCTTTCCATGGGTCTTTTTCGACGTACC	10447
RESULT 15 .				
ID	ADE06462			
XX	ADE06462 standard; DNA; 10447 BP.			
AC	ADE06462;			
XX				
DT	29-JAN-2004 (first entry)			
XX				
DE	Vector pGal/IC25.			
XX				
KM	HIV infection; Anti-HIV; vaccine; ds.			
OS	Synthetic.			
FT				
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Key				
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PR	03-JAN-2003; 2003US-00336566.		
PA	(UYEM-) UNIV EMORY.		
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.		
PI	Robinson HL, Smith J, Hua J, Moss B;		
DR	WPI; 2003-731822/69.		
XX			
XX			
XX	A composition for generating an immune response against HIV comprises a vector comprising a vaccine insert encoding one or more antigens that elicit an immune response against HIV.		
PT			
PT			
PS	Example 11; Fig 13; 133pp; English.		
CC	The present invention relates to a composition comprising a first vector with a vaccine insert encoding one or more antigens that elicit an immune response against HIV or a first subtype or recombinant form; and a second vector comprising a vaccine insert encoding one or more antigens that elicit an immune response against an HIV of a second subtype or recombinant form. The composition is useful in generating an immune response against HIV. The insert of the first vector or the insert of the second vector comprises the sequences of two or more of: a gag, pol, env, tat, rev, nef, vif, vpr or vpu gene; or their mutants, and optionally, non-coding regulatory sequences of the HIV genome. At least one of the two or more sequences comprises mutations that limit the encapsidation of viral RNA, or a gag sequence having a mutation in one or more of the sequences encoding a zinc finger. All or part of cis-acting RNA encapsidation sequences have been deleted from the non-coding regulatory sequences of HIV-1. The two or more sequences comprise a pol sequence having a mutation that inhibits one or more of the enzymatic activities of pol. The enzymatic activity is integrase activity, reverse transcriptase activity or protease activity. The enzymatic activity is inhibited by deleting a portion of the pol sequence or introducing one or more point mutations into the pol sequence. The present sequence is one such vector used to illustrate the invention.		
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Query Match	31.6%; Score 2027.2; DB 9; Length 10447;		
Best Local Similarity	87.4%; Pred. No. 0;		
Matches 2406; Conservative	1; Mismatches 14; Indels 331; Gaps 4;		
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DB	8024 ACTGGCTTTCTACGCGAAAAGACTCTGAGTAACATCCTTTTTGTATATCATGACC	8083	
OY	1714 AATCCCTTAA CGTAGTGTTTCGTTCACTGAAGCTCACGCCCGTAGA AAAAGATCAAAG	1773	
DB	8084 AATCCCTTAA CGTAGTGTTTCGTTCACTGAAGCTCACGCCCGTAGA AAAAGATCAAAG	8143	
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DB	8144 ATCTTTCTTGAGATCCTTTTTTTCTGCGCGCTAATCTGCTGTGCAACA CA AA AACACACC	8203	
OY	1834 GTACACAGCGGTGCTTTGTGTCGCAGATCAAGA CTACCAACTCTTTTCCGAGGTAA C	1893	
DB	8204 GTACACAGCGGTGCTTTGTGTCGCAGATCAAGA CTACCAACTCTTTTCCGAGGTAA C	8263	
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QY      2074  GGTAAAGGCGGAGCGGTGCGGCTGAACGGGGGTTGCTGCAACAGCCAGCTTGGAGCG 2133
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GenCore version 5.1.6
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34: em_hcg_pln:*
35: em_hcg_rod:*
36: em_hcg_mam:*
37: em_hcg_vtc:*
38: em_sy:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	2878.4	44.9	5386	6	AX743953	AX743953 Sequence
C 2	2878.4	44.9	7036	6	AX743955	AX743955 Sequence
C 3	2878.4	44.9	7334	6	AX743956	AX743956 Sequence
5	2378.8	37.1	5089	6	AX776820	AX776820 Sequence
6	2378.8	37.1	5089	6	AX776823	AX776823 Sequence
7	2378.8	37.1	5488	6	AX776821	AX776821 Sequence
8	2378.8	37.1	5488	6	AX776824	AX776824 Sequence
9	2378.8	37.1	5500	6	AX776819	AX776819 Sequence
10	2020.8	31.5	9918	12	AF430344	AF430344 Synthetic
11	2008.6	31.3	5108	6	AX138932	AX138932 Sequence
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14	2008.6	31.3	5108	6	BD000658	BD000658 Growth ho
15	2008.6	31.3	5111	6	AX138936	AX138936 Sequence
16	2008.6	31.3	5111	6	BD000701	BD000701 Growth ho
17	2008.6	31.3	5185	6	AX138928	AX138928 Sequence
18	2008.6	31.3	5185	6	BD000693	BD000693 Growth ho
19	2008.6	31.3	5188	6	AX138940	AX138940 Sequence
20	2008.6	31.3	5188	6	BD000705	BD000705 Growth ho
21	2008.6	31.3	5254	6	AX138941	AX138941 Sequence
22	2008.6	31.3	5254	6	BD000706	BD000706 Growth ho
23	2000.8	31.2	11358	6	BD000820	BD000820 Compositi
24	1965.2	30.7	5899	6	AR231272	AR231272 Sequence
25	1955.6	30.5	7528	6	AX080953	AX080953 Sequence
26	1942.2	30.3	5845	6	AR231271	AR231271 Sequence
27	1892.2	29.5	2041	6	AX285154	AX285154 Sequence
28	1890.8	29.5	1894	6	AR004653	AR004653 Sequence
29	1890.8	29.5	1894	6	AR062126	AR062126 Sequence
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36	1886.4	29.4	1888	9	HSTYROR	Y08819 Human mRNA
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38	1885	29.4	1906	6	I17316	I17316 Sequence 1
39	1885	29.4	1910	6	AR061264	AR061264 Sequence
C 40	1855.4	29.0	5874	6	AX615156	AX615156 Sequence
C 41	1855.4	29.0	5875	6	AX754988	AX754988 Sequence
C 42	1852.2	28.9	1920	6	I70156	I70156 Sequence 7
C 43	1814.4	28.3	6407	6	I31847	I31847 Sequence 1
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C 45	1784.6	27.8	229483	14	AC146851	AC146851 Human Her

ALIGNMENTS

RESULT 1
AX743953/c
LOCUS AX743953 5386 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 1 from Patent WO03031630.
ACCESSION AX743953
VERSION AX743953.1 GI:30722650
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Fazio,V., Rinaldi,M., Sonzogni,L., Tonon,G. and Oresini,G.
Multi-clonronic vectors for gene transfer protocols
Patent: WO 03031630-A 1 17-APR-2003;
Keryos Spa (IT)

FEATURES
source Location/Qualifiers
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/db_xref="taxon:32630"

Query Match 44.9%; Score 2878.4; DB 6; Length 5386;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 3354; Conservative 0; Mismatches 201; Indels 285; Gaps 7;

ORIGIN
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5381 TTGAAAACTCATCGACATCAAAATGAAATGCAATTTATTCATATCAGATTATCAAT 5322
645 ACCATATTTTGAAGAGCGTTTCTGTATGAAAGAAACTCCGACGAGAGTTCCA 704
5321 ACCATATTTTGAAGAGCGTTTCTGTATGAAAGAAACTCCGACGAGAGTTCCA 5262
705 TAGGATGCGAAGATCCTGTATCGATCTGCGATTCCGATCTGTCACATCAATCAAC 764
5261 TAGGATGCGAAGATCCTGTATCGATCTGCGATTCCGATCTGTCACATCAATCAAC 5202
765 TATTAATTTCCCTCGTCAAAAATTAAGTTATCAAGTGAATAATCACATGAGTGAAG 824
5201 TATTAATTTCCCTCGTCAAAAATTAAGTTATCAAGTGAATAATCACATGAGTGAAG 5142
825 TGAATCCGGTGAATGGCAAAAGCTTATGCAATTTCTTTCGACATTTTCAACAGGCA 884
5141 TGAATCCGGTGAATGGCAAAAGCTTATGCAATTTCTTTCGACATTTTCAACAGGCA 5082
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2501 AATTACGGGGTATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 2557
3719 GAGCGGAAAGACAGAGCGGACAGAGTCAAGTACGAGAGGAGAGGCGGCAATAC 3660
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QY	2618	GAGATCTGATTTAGTGTGACAGACATATAGAGCTATATCGCCATTAAGGAGCATCAAG	2617
Db	3599	CCGACGTGAAGACGGCGCGTAGGCGCAACGCAATTAATGTGAGTTAGCTCACTCATTAAGG	3540
QY	2678	C-----TGGCAGCATGGCCAAATGCAATTCAGTCACTTGAATCAATATG3--	2725
Db	3559	CACCCAGGCTTTACACTTTATGCTTCGGGCTCGTATGTTGTGGAAATGTGAGCGGAT	3480
QY	2726	--CAATTAGCCATATTAGTCATTGGTATATATAGCATTAATCAATATTTGGCT----	ATT 2777
Db	3479	AACAATTTCAACAGGAAACAGCTATGACCATGATTAAGCCAGCTTGCAATGCTGCGAGT	3420
QY	2778	GGCCATTGCGATAGCTGTTGATCTATATCATTAATATGTACATTTATATTTGGCTCANGTCCA	2837
Db	3419	GGCCATTGCGATAGCTGTTGATCTATATCATTAATATGTACATTTATATTTGGCTCANGTCCA	3360
QY	2838	TATACCGCCCATGTTGACATGATTAATTAATGACTAGTTATATATAGTAATCAATTAACGGGGT	2897
Db	3359	CATTACCGCCCATGTTGACATGATTAATTAATGACTAGTTATATATAGTAATCAATTAACGGGGT	3300
QY	2898	CATTAGTTTCATAGCCCATATATATGAGAGTTCCGCGTTACATTACTTAACGGTAATAGCCCGC	2957
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QY	2958	CTGGCTGACGCGCCAAACGACCCCGCCCATTTGACGTCATAGTATGACGTATGTTCCCATAG	3017
Db	3239	CTGGCTGACGCGCCAAACGACCCCGCCCATTTGACGTCATAGTATGACGTATGTTCCCATAG	3180
QY	3018	TAAAGCCCATATAGGGACTTTCCATTGAGCTCAATGGGTGGAGTATTTACGGTAATCTGCC	3077
Db	3179	TAAAGCCCATATAGGGACTTTCCATTGAGCTCAATGGGTGGAGTATTTACGGTAATCTGCC	3120
QY	3078	ACTTGGCGAGTACATCAAGTGTATCATATAGCCAAAGTCGCGCCCTATTGACGTCAATGACG	3137
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QY	3198	AGTACATTTACGATTAATAGTCATTCGCTATTATACCATGTGTATGTCGGTTTTGGCAGTACACA	3257
Db	2999	AGTACATTTACGATTAATAGTCATTCGCTATTATACCATGTGTATGTCGGTTTTGGCAGTACACA	2940
QY	3258	ATGGGCGGTGAATAGGGGTTGACACAGGGGATTTCCAAAGTCTCACCCCATTTAGACGTCA	3317
Db	2939	ATGGGCGGTGAATAGGGGTTGACACAGGGGATTTCCAAAGTCTCACCCCATTTAGACGTCA	2880
QY	3318	ATGGGAGTTGTTTGGCAGCCAAATCAACGGGACTTCCAAATATGTGTATTAACCCCG	3377
Db	2819	ATGGGAGTTGTTTGGCAGCCAAATCAACGGGACTTCCAAATATGTGTATTAACCCCG	2820
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Db	2819	CCCCATTTAGCCAAATGGGCGGTAGCGGTGTACGGTGGGAGGTCTATATTAAGCAGAGCTC	2760
QY	3438	GTTTATAGTAAACCGTCAAGTTCGCTGTGAGAACGCCATCCACGCTGTTTGAACCTCCATAGAA	3497
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Db	2639	GTCGCAAGAGTGACGTAAAGTACCGCTATAGAGTCTATAGGCACACCCCTTTGGCTCTTA	2580
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Db	2579	TGCATGCTATACCTGTTTTGGTTGGGCGCTATACACCCCGCTTCTTATGCTATAGT	2520

QY	3678	GATGTAATAGCTTGGCCTAATAGGGGGTATTGACATTATTGACACTCCCTATTG	3737
Db	2519	GATGTAATAGCTTGGCCTAATAGGGGGTATTGACATTATTGACACTCCCTATTG	2460
QY	3738	GTGACGATACTCTTCATTAATCAATCCATAATGAGCTCTTTGGCACAACATCTCTATTG	3797
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QY	3858	GGGTGCCCATTTATTATTTCACAAATTCACATATATAACAAGCCCGTCCCCCGTGGCCGACG	3917
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Db	2279	TTTTTATTTAAACATAGGGTGGGATCTCAAGCCGAATCTCGGGTACGATTCCTCCGACATGG	2220
QY	3978	GCTCTTCTCCGGTAGCGGCGGAGCTTCCACATCCGAAGCCGTGGTCCCATGCTTCCAGACGG	4037
Db	2219	GCTCTTCTCCGGTAGCGGCGGAGCTTCCACATCCGAAGCCGTGGTCCCATGCTTCCAGACGG	2160
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QY	4098	AATGCCCCACACACCAATGTGCCGACCAAGGCCGTGGCGGTAAAGGATATGTCTGAAAA	4157
Db	2099	AATGCCCCACACACCAATGTGCCGACCAAGGCCGTGGCGGTAAAGGATATGTCTGAAAA	2040
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Db	2039	TGAGCTGGGAATTTGGGCTGCGCACGCGTGACGAGATGGAAGATTAAAGGACGCGGACGA	1980
QY	4218	AGAAAGTACAGGACAGCTGATGTTGTTGTAATCTGATTAAGAATCAGAGGTAACTCCCGTTGC	4277
Db	1979	AGAAAGTACAGGACAGCTGATGTTGTTGTAATCTGATTAAGAATCAGAGGTAACTCCCGTTGC	1920
QY	4278	GGTGTGTTAAACGGTGAAGGGCAGTGTAGTCTGAGCAATCTGTTGCTGCGCGCGCGC	4337
Db	1919	GGTGTGTTAAACGGTGAAGGGCAGTGTAGTCTGAGCAATCTGTTGCTGCGCGCGCGCGC	1860
QY	4338	CACCAAGATATATAGCTGACAGACTTAAACAAGCTGTTCTTTCCATGGGTCTTTTCACAG	4397
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LOCUS	AX743955/c	7086 bp	DNA	linear	PAT 14-MAY-2003
DEFINITION	AX743955				
SEQUENCE	Sequence 3 from Patent WO03031630.				
ACCESSION	AX743955				
VERSION	AX743955.1	GI:30722652			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE	1				
AUTHORS	Fazio, V., Rinaldi, M., Sonzogni, L., Tonon, G. and Orsini, G.				
TITLE	Multi-electronic vectors for gene transfer protocols				
JOURNAL	Patent: WO 03031630-A 3 17-Apr-2003;				
	Keryos Spa (IT)				
FEATURES					
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ORIGIN					
Query Match	44.9%	Score 2878.4	DB 6	Length 7086	
Best Local Similarity	87.3%	Pred. No. 0			

Matches 3354; Conservative 0; Mismatches 201; Indels 285; Gaps 7;

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QY	645	ACCATATTTTGGAAAAAGCCGTTTCTGTAAATGAAGAGAAAACTCACGAGGAGTTTCCA	704
Db	7021	ACCATATTTTGGAAAAAGCCGTTTCTGTAAATGAAGAGAAAACTCACGAGGAGTTTCCA	6962
QY	705	TAGAGATGGCAAGATCTCGTATTCGGTCTGCGAATTCGACCTGTGTCCAAATCAATACCAAC	764
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Db	6901	TATTAATTTTCCCTCGTCAAAAATPAAGTTTATCAAGTAGAGAAATCACCATGATGACGAC	6842
QY	825	TGAATCCGGTGAAGATGGCAAAAGCTTATGCAATTTCTTCCAGACTGTGTCAACGCGCA	884
Db	6841	TGAATCCGGTGAAGATGGCAAAAGCTTATGCAATTTCTTCCAGACTGTGTCAACGCGCA	6782
QY	885	GCCATTGCGCTCGATCACTAAAAATCACTCGCATCAACCAACCGTATTCATTCGGGATGG	944
Db	6781	GCCATTGCGCTCGATCACTAAAAATCACTCGCATCAACCAACCGTATTCATTCGGGATGG	6722
QY	945	CGCCTGACCGAGCAAAATAGCGATCGCTTTAAAGACAATTAACAACAGAAATCGA	1004
Db	6721	CGCCTGACCGAGCAAAATAGCGATCGCTTTAAAGACAATTAACAACAGAAATCGA	6662
QY	1005	ATGCAACCGGGCGAGAACTATGCAAGGCAATCAATATTTTCACTGAAATCAGATA	1064
Db	6661	ATGCAACCGGGCGAGAACTATGCAAGGCAATCAATATTTTCACTGAAATCAGATA	6602
QY	1065	TTCTTTCTAATACCTGAGATCGTGTTCCTCCGGGAGTCGACAGTGTGAGTAACCATGCATC	1124
Db	6601	TTCTTTCTAATACCTGAGATCGTGTTCCTCCGGGAGTCGACAGTGTGAGTAACCATGCATC	6542
QY	1125	ATCAGAGATACGATTAATAATCTTGATGTGTGGAAGAGGCAATAATTCGTACGCMGTT	1184
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Db	6361	ATTATTCGGAGACCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGG	6302
QY	1365	CCTCGAGCAAGCGTTTCCGTTGAATATGCTCATTAACCCCTGTGATTAACGTTAT	1424
Db	6301	CCTCGAGCAAGCGTTTCCGTTGAATATGCTCATTAACCCCTGTGATTAACGTTAT	6242
QY	1425	GTAAGCAAGACGTTTATTTGTCATGATGATATATTTTATCTGTGTGCAATGTAAATCA	1484
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QY	1485	GAGATTTTGAACAACAATGTGGCTTTCCCCCCCCCCTGCAAGGCTTCTTCTTTTCCC	1544
Db	6220	-----	6221
QY	1545	CACCCCAACCCCAAGTTCCGGGTGAAGGCCGAGGCTCGACCAACGTCCGGGCGCGAG	1604
Db	6220	-----	6221
QY	1605	GCCCTGCCATAGCTCAGGTTATCTCATATATATCTTTAGATGATTTAAACTTCATTTT	1664
Db	6220	-----	6221

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Db	6220	-----TATGACCAAAATCCCTTAAC	6260
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QY	1785	ATGCTTTTTCGAGCGGATCTGTCGTGTCGCAAAACAAAACCAACCGGTACAGGGG	1844
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QY	1845	TGGTTTGTTCGCGGATCAAGAGCTAACCAACTCTTTTTCGAAAGTAACTGCTTCAGCA	1904
Db	6079	TGGTTTGTTCGCGGATCAAGAGCTAACCAACTCTTTTTCGAAAGTAACTGCTTCAGCA	6020
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Db	6019	GACCGCAGATACCAATATCTGTTCTTCTTAAGTATACCGTAACTGTAAGCCACACTTCAGA	5960
QY	1965	ACCTGTAGACGCGCTTACATACCTCGCTGCTCTATCCTGTATCCAGT---GCTGCTG	2021
Db	5959	ACCTGTAGACGCGCTTACATACCTCGCTGCTCTATCCTGTATCCAGTGGCTGCTGCTG	5900
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Db	5899	CGAGTGGCAATAGTCGTGTCCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAGG	5840
QY	2082	CGAGAGGTCGCGGCTGACGGGGGGGTGCTGACACCCAGCGTGGAGGGAACGACCT	2141
Db	5839	CGAGAGGTCGCGGCTGACGGGGGGGTGCTGACACCCAGCGTGGAGGGAACGACCT	5780
QY	2142	ACACCGAATGAGATACCTTACAGCGTGAATATGAGAAAGCGCACGCTTCGAGGGGA	2201
Db	5779	ACACCGAATGAGATACCTTACAGCGTGAATATGAGAAAGCGCACGCTTCGAGGGGA	5720
QY	2202	GAAAGCGGACAGGTATCCGGTAAACGGGCGAGGGTGGAAACAGGAGCGGACAGGGAGC	2261
Db	5719	GAAAGCGGACAGGTATCCGGTAAACGGGCGAGGGTGGAAACAGGAGCGGACAGGGAGC	5660
QY	2262	TTCCAGGGGGAAACCGCTGTAATCTTATATAGTCCTGTGGGTTTGCCACCTCGACTTG	2321
Db	5659	TTCCAGGGGGAAACCGCTGTAATCTTATATAGTCCTGTGGGTTTGCCACCTCGACTTG	5600
QY	2322	AGCGTCGATTTTGTGATCTCTGTCAGGGGGGCGGAGCCTATGAAAAACCCAGCAACG	2381
Db	5599	AGCGTCGATTTTGTGATCTCTGTCAGGGGGGCGGAGCCTATGAAAAACCCAGCAACG	5540
QY	2382	CGGCTTTTTCACGCTTCGAGCCTTTTGCTGGCCCTTTTGCTCAAGTTCCTTCCTGGCT	2441
Db	5539	CGGCTTTTTCACGCTTCGAGCCTTTTGCTGGCCCTTTTGCTCAAGTTCCTTCCTGGCT	5480
QY	2442	TATCCCTGATTTTGATGATTAACCGTATTAACCGGC--ATGCATTAAGTTTAAATAGTATC	2500
Db	5479	TATCCCTGATTTTGATGATTAACCGTATTAACCGCTTTGATGAGTGAATACCGCTGCC	5420
QY	2501	AATTACGGGCTCATTAAGTTCATAGCCCATATATGAGATTCGCGCTTACATAAC---TTAC	2557
Db	5419	GACGCGGAACGACCGAGCCAGCGATCGATAGGAGGAAGCGGAAGCGCCCAATAC	5360
QY	2558	GGTAAATAGCGCGCTGAGCGGCGCCACGACCCCGCCCATATGAGTCAATATATGAC	2617
Db	5359	GCAAACGCTCTTCCCGCGCGCTTGGCCATTTAATGACGCTGGGACAGCAGGTTTC	5300
QY	2618	GAGATCTGATATAGTGACAGACGATATGAGCTATATCGCCGATGAGGCGCATATCAG	2677
Db	5299	CCGACTGAAAGCGGGCAGTAGCGCAACGCAATTAATGTAGTTAGCTCATATAGG	5240
QY	2678	C-----TGGCACATGGCCATGCTATTCGATCTATACATTAATTG--	2725
Db	5239	CACCCAGGCTTTAACCTTATGCTTCGGCTGCGATGTTGTGGAAATGTGAGCGGAT	5180

QY	2726	--CAATTAGCCAAATTATTCATCTGGGTATATAGCAATAATCAATATGGCT-----ATT	2777
Db	5179	AACAATTTTCAACAAGAAAACAGCTATGACCATGATTTAGCCAAAGCTTGCAAGCTCGCACT	5120
QY	2778	GGCCATTGGCAACGTTGTATCTATATCAATAATATGACATTTATATTTGGCTCATGTCCAA	2837
Db	5119	GGCCATTGCAATACGTTGTATCTATATCAATAATATGACATTTATATTTGGCTCATGTCCAA	5066
QY	2838	TATGACCGCCCATGTTGACATTTGATTTATGACTGATTTAATAGTAATCAATTAACGGGT	2897
Db	5059	CATTACCGCCCATGTTGACATTTGATTTATGACTGATTTAATAGTAATCAATTAACGGGT	5000
QY	2898	CATTAGTTCAATAGCCCATATATGAGAGTTCCCGCTTACATTAACCTTAACGGTAATGGCCCG	2957
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QY	2958	CTGGCTGACCGCCCAACGACCCCGCCCATTTGACGTCATATGATGACGATGTGCCCATAG	3017
Db	4939	CTGGCTGACCGCCCAACGACCCCGCCCATTTGACGTCATATGATGACGATGTGCCCATAG	4880
QY	3018	TAAAGCCCAATAGGGACTTTTCATTGACGTCATATGAGGTGAGATATTTACGGTAAACCTGCCC	3077
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QY	3078	ACTTGGCAGTACATTAAGTGATATCATATGCCAATGTCGCCGCCCTTATGAGCTCAATGACG	3137
Db	4819	ACTTGGCAGTACATTAAGTGATATCATATGCCAAGTACCCCTCTATATGACGTCATATGACG	4760
QY	3138	GTAATATGCCCCGCCCTGGCAATTATGCCCCAGTACATGACCTTACCGGGACTTTCTACTTGGC	3197
Db	4759	GTAATATGCCCCGCCCTGGCAATTATGCCCCAGTACATGACCTTACCGGGACTTTCTACTTGGC	4700
QY	3198	AGTACATTAAGTATTTATTCATCTGCTATTAACATGATGATGCGGTTTTGGCAGTACACCA	3257
Db	4699	AGTACATTAAGTATTTATTCATCTGCTATTAACATGATGATGCGGTTTTGGCAGTACATCA	4640
QY	3258	ATGGGCGTGATACGCGGTTTGACTCAACGGGAATTTCAGATCTCCACCCATTGACGTCA	3317
Db	4639	ATGGGCGTGATACGCGGTTTGACTCAACGGGAATTTCAGATCTCCACCCATTGACGTCA	4580
QY	3318	ATGGGAGTTTTGTTTGGCAACCAAAATCAACGGGACTTTCCAAATATGCTAATAACCCG	3377
Db	4579	ATGGGAGTTTTGTTTGGCAACCAAAATCAACGGGACTTTCCAAATATGCTAATAACCCG	4520
QY	3378	CCCCGTTTACGCAAAATGGCGGTTAGCGCTGTATACGGTGGAGGCTTATATAGCAGAGCTC	3437
Db	4519	CCCCGTTTACGCAAAATGGCGGTTAGCGCTGTATACGGTGGAGGCTTATATAGCAGAGCTC	4460
QY	3438	GTTTATGTGAACCGTCAGATTCGCTTGAGAGCGCATCAACGCTGTTTGGACCTCCATAGAA	3497
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QY	3558	GTGCGCAAGTGAAGTAAAGTACCGGCTTATAGCTTATAGGCAACACCCCTTTGGCTCTTA	3617
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QY	3618	TGCATGCTATATCTGTTTTTGGCTTGGGGCTATACACCCCGGCTTCTTATGCTATAGGT	3677
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QY	3678	GATGTTATATGCTTAACTTATAGCTTATAGCTGTGGGTTATTTGACATTTATGACCACTTCCCTATTTG	3737
Db	4219	GATGTTATATGCTTAACTTATAGCTTATAGCTGTGGGTTATTTGACATTTATGACCACTTCCCTATTTG	4160
QY	3738	GTGACGATATCTTCCATTAATCAATCAAAACATGCGCTTTTGGCCACAATCTCTATTTG	3797
Db	4159	GTGACGATATCTTCCATTAATCAATCAAAACATGCGCTTTTGGCCACAATCTCTATTTG	4100
QY	3798	GCTATATGCCAAATATCTGTCTCTTCAGAGACTGACACGGACTGTGATTTTTTATACAGATG	3857

Db	4099	GCTATATGCCAATBCTCTGTCTCTTCAGAGACTGACACGCACTGTGTAATTTTACAGATG	4040
Qy	3858	GGGTGCCATTATTTATTTAACAAATTCACATATACAAACAACGCCGTCCCGTGCCGCGAG	3917
Db	4039	GGGTCCCATTTATTTATTAACAAATTCACATATATACAAACAACGCCGTCCCGTGCCGCGAG	3980
Qy	3918	TTTTTTATTTAAACATAGCGTGGGATCTCCACGCCAATCTGGGGTACGTGTTCCGGACATGG	3977
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Qy	3978	GCTCTTCGCCGATGAGCGCGGAGGCTTCACATCCAGACCCCTGGGCCCATGCTCCACAGCG	4037
Db	3919	GCTCTTCTCCGGTAGCGCGGAGGCTTCACATCCAGACCCCTGGTCCATGCTCCACAGCG	3860
Qy	4038	CTCATGTGTGCTCGGCGACTCTTGTCTCTTAACAGTGGAGGCGCACTTAAGGACACAGCAC	4097
Db	3859	CTCATGTGTGCTCGGCGACTCTTGTCTCTTAACAGTGGAGGCGCACTTAAGGACACAGCAC	3800
Qy	4098	AATGCCACCAACCAACCAAGTGTCCGCAACAAGCGCGTGGGATATGTGTCTGAAAA	4157
Db	3799	AATGCCACCAACCAACCAAGTGTCCGCAACAAGCGCGTGGGATATGTGTCTGAAAA	3740
Qy	4158	TGAGCTGGAGATTGGGCTGGCACCGCTGACGGCAGATGAGAACTTAAGGACAGCGCAGA	4217
Db	3739	TGAGCTGGAGATTGGGCTGGCACGGCTGACGGCAGATGAGAACTTAAGGACAGCGCAGA	3660
Qy	4218	AGAAGATGACAGGCACTGAGTGTGTTGATTTCTGATAAGATCAGAGGTAATCCCGTTGC	4277
Db	3679	AGAAGATGACAGGCACTGAGTGTGTTGATTTCTGATAAGATCAGAGGTAATCCCGTTGC	3620
Qy	4278	GGTCTGTGTAACGGGTGAGGGGCACTGATGTCAGACGTACTCGTTGCTCCGCGCGCGC	4337
Db	3619	GGTCTGTGTAACGGGTGAGGGGCACTGATGTCAGACGTACTCGTTGCTCCGCGCGCGC	3560
Qy	4338	CACCAAGCATTAATAGCTGACAGACTAACACACTGTTCTTTCCATGGGTCTTTTCTGCA	4397
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VERSION	AX743956.1	GI:30722653	
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SOURCE			
ORGANISM			
REFERENCE			
AUTHORS	Fazio, V., Rinaldi, M., Sonzogni, L., Tomon, G. and Orsini, G.		
TITLE	Multi-electronic vectors for gene transfer protocols		
JOURNAL	Patent: WO 03031630-A 4 17-APR-2003;		
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Best Local Similarity	87.3%;	Pred. No. 0;	
Matches 3354;	Conservative 0;	Mismatches 201;	Indels 285; Gaps 7;
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Db	7329	TTAGAAAACTCATCGAGCATCAATGAAACTGCAATTTATTCATATCAGGATTTATCAAT	7270
Qy	645	ACCAATATTTTGAAGAAAGCGTTTCTGTATGGAAGGAAACCTCAGGAGGCGAGTTTCA	704
Db	7269	ACCAATATTTTGAAGAAAGCGTTTCTGTATGGAAGGAAACCTCAGGAGGCGAGTTTCA	7210

QY	705	TAGAGTGGCAGAGATCTCTGGTATCCGTCTCGCATTTCCACTCTGTCCAACTCAATACCAACC	764
Db	7209	TAGAGTGGCAGAGATCTCTGGTATCCGTCTCGCATTTCCACTCTGTCCAACTCAATACCAACC	7150
QY	765	TATTATATTTCCCTCTGTCGTAATAATTAAGGTATATCAAGTGAAGAAATCACATGAGTGAAGAC	824
Db	7149	TATTATATTTCCCTCTGTCGTAATAATTAAGGTATATCAAGTGAAGAAATCACATGAGTGAAGAC	7090
QY	825	TGAATCCGGTGAAGATGGCAAAAGCTTATGCAATTTCTTTCCAGACTTGTTCAACAGGCA	884
Db	7089	TGAATCCGGTGAAGATGGCAAAAGCTTATGCAATTTCTTTCCAGACTTGTTCAACAGGCA	7030
QY	885	GCCATTACGCTCTGTCATCAAAATCACTGGCATCAACCAACCCGTTATTCATTGCTGATG	944
Db	7029	GCCATTACGCTCTGTCATCAAAATCACTGGCATCAACCAACCCGTTATTCATTGCTGATG	6970
QY	945	CGCCTGACGAGACGAATAACGCCATGCTGTTAAAGACAATTAACAAACAGAAATCGA	1004
Db	6969	CGCCTGACGAGACGAATAACGCCATGCTGTTAAAGACAATTAACAAACAGAAATCGA	6910
QY	1005	ATGCAACCGGCGCAGAGAACTCTGCAGCGCATCAACAATATTTTCACTGTATCAGATGA	1064
Db	6909	ATGCAACCGGCGCAGAGAACTCTGCAGCGCATCAACAATATTTTCACTGTATCAGATGA	6850
QY	1065	TTCTTCTAATACCTGGAAATGCTGTTTCCCGGGGATCGCATGCTGATGAATCAATGCATC	1124
Db	6849	TTCTTCTAATACCTGGAAATGCTGTTTCCCGGGGATCGCATGCTGATGAATCAATGCATC	6790
QY	1125	ATCAGAGATACGGATAAATATGCTGATGCTGTGGAGAAAGGCAATTAATCCGACAGCT	1184
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QY	1185	TAGTGTGACCAATCTCATCTGTAACTCATCTTGGCAGCGTACCTTTGCCATGTTTCAGAAA	1244
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QY	1245	CAACTCTGCGCATCGGCTTCCCATCAATCATGATGATGTCGCACTGTATGCCCGAC	1304
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QY	1305	ATTATCGGAGGCCAATTTATACCCATATTAATACAGCATCAATGTTGAATTATACCGG	1364
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QY	1365	CCTCGAGCAAGACGTTTCCCGTGGATATGCTCATTAACCCCTGTATTAATCTGTTAT	1424
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QY	1425	GTAAAGCAAGCACTTTTATTTTCATGATGATATATTTTATTTCTGTGCAATGTAACATCA	1484
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QY	1485	GAGATTTTGAAGACAACAAGTGGCTTTCCCCCCCCCCCCCTGCAAGGCTTTCTTCTTTCCC	1544
Db	6468	-----	6469
QY	1545	CACCCACCCCCCAAGTTGCGGTTGAAGGCCAGGCTGCAAGCAAGTCGCGGCGGAG	1604
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QY	1605	GCCCTGCATAGCTCAAGTTACTCATATATACCTTTAGATTGATTTAAACCTCATTTTT	1664
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QY	1665	AATTTAAAGATCTAGGTGAAGATCTTTTGTATATCTCATGACCAAAATCCCTTAAC	1724
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QY	1725	GTGATTTTTCGTTCCATGAGGCTGAGACCCCGTGAAGAAAGATCAAAAGATCTTCTTAG	1784
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QY	1785	ATCCCTTTTTCTGGGGGTAATCGTCGCTTGGCAAAACAAAACCAACCGCTACAGCGG	1844
Db	6387	ATCCCTTTTTCTGGGGGTAATCGTCGCTTGGCAAAACAAAACCAACCGCTACAGCGG	6328
QY	1845	TGTTTGTGTTGGCCGGATCAAGAGCTACCAACTCTTTTTCGGAAGTAATTGGCTTCAGCA	1904
Db	6327	TGTTTGTGTTGGCCGGATCAAGAGCTACCAACTCTTTTTCGGAAGTAATTGGCTTCAGCA	6268
QY	1905	GAGCGCAGATACCAAAATCTGTCTTCTTAAGTGAACCCGTAGTTAGGCCACACTTCACAGA	1964
Db	6267	GAGCGCAGATACCAAAATCTGTCTTCTTAAGTGAACCCGTAGTTAGGCCACACTTCACAGA	6208
QY	1965	ACTCTGTAGACAACCGCCTACAACTCGCTCGCTAACCTCTGTACCAAGTG---GCTGCTG	2021
Db	6207	ACTCTGTAGACAACCGCCTACAACTCGCTCGCTAACCTCTGTGTACCAAGTGCTGCTGCTG	6148
QY	2022	CCAGTGGCGATAAGTCCGTGCTTACCGGGGTTGAGCTCAAGACGATGTTACCGGATTAAG	2081
Db	6147	CCAGTGGCGATAAGTCCGTGCTTACCGGGGTTGAGCTCAAGACGATGTTACCGGATTAAG	6088
QY	2082	CGCAGCGGTGGGGCTGAACGGGGGGTTCTGTGACACAGCCCAAGCTTGAAGCAAGCACT	2141
Db	6087	CGCAGCGGTGGGGCTGAACGGGGGGTTCTGTGACACAGCCCAAGCTTGAAGCAAGCACT	6028
QY	2142	ACACCGGAATGAAATCCTACAGGTGAGCTATGAGAAAGGCCACCGCTTCCGGAAGGA	2201
Db	6027	ACACCGGAATGAAATCCTACAGGTGAGCTATGAGAAAGGCCACCGCTTCCGGAAGGA	5968
QY	2202	GAAAGGCGGACAGGTATCCGGTAAAGCGGACGAGGCTCGAAACAGAGACGCGACGAGGAGC	2261
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QY	2262	TTCCAGGGGGAAACCGCTGTATCTTTATAGTCTGTGCGGGTTTCGCCACTCTGACTTG	2321
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QY	2322	AGCGTCGATTTTTGTATGCTCTGTCAGGGGGGGCGAAGCTATGGAACAAACGCCAGCAAGC	2381
Db	5847	AGCGTCGATTTTTGTATGCTCTGTCAGGGGGGGCGAAGCTATGGAACAAACGCCAGCAAGC	5788
QY	2382	CGGCGCTTTTACGGTCCCTGGCCCTTTTGCTGGCCCTTTTGGCTCAATGTTCTTCTCGCGT	2441
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QY	2442	TATCCCTCGATTCGTGTGATTAACCGTATTAACCGCC-ATGCAATTAGTTAATAGTATC	2500
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QY	2501	AATTACGGGGTCATTAGTTCATAGCCATATATGAAAGTTCCGCGCTACATAAC--TTAC	2557
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QY	2558	GSTAAATGGCCCGCTGGCTGACCGGCCCAACGACCCCGCCCATTTGACGTCAATATGAC	2617
Db	5607	GCAAAACCGCTCTCCCGCGCGCTGGCCGATTCACTTAATGCAAGCTGGCAGACAGGTTTC	5548
QY	2618	GAGATCTGATTAAGTGCACACGATATGAGGCTATATCCGCGATAGAGGCGACATCAAG	2677
Db	5547	CCGACTGGAAGCGGGCAGTGAAGGCGAACGCAATTAATGTGAGTTAGCTCACTCATTAAG	5488
QY	2678	C-----TGCGACATGGCCCAATGATCATATCATATCATTAATCAATATTGG--	2725
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QY	2778	GGCCATTCGATACGTTGATCTATATCATATCATATATGATACATTAATTGGCTCATGTCGA	2837
Db	5367	GGCCATTCGATACGTTGATCTATATCATATCATATATGATACATTAATTGGCTCATGTCGA	5308
QY	2838	TATGACCGCAATGTTGACATTTGATTAATGACTTAATTAATGATTAATCAATTAACGGGT	2897

Db	5307	CATTACCGCCAGTTGACATTGATTATTAAGTACTGTTATTAATGAAATCAATTAACGGAGT	5248
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Db	5247	CATTAGTTCAATAGCCCATATATAGAGTTCGCGCTTACATTAACCTTAACGTAATGGCCGC	5188
Oy	2958	CTGGCTGACCGCCCAACGACCCCGCCATTGACGTCATATGATGACGTATGTTCCATAG	3017
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Oy	3018	TAAAGCCAAATAGGACCTTTCATATGACGTCAAATGGGTGGAATATTTCACGTAACCTGCC	3077
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Oy	3078	ACTTGGCGAGTACATCAAGTGTATCATATGCGCAAGTCGCGCCCTATTGACGTCATATGACG	3137
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Oy	3138	GTAATAGCGCGCGCTGGCATTAATGCCAGTACATGACCTTACGGGACCTTCTACTTGGC	3197
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Oy	3198	AGTACATCTACGATTAATGATCATTCGCTATTACATGCTATATGCGGTTTGGCAGTACACA	3257
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Oy	3498	GACACCGGGACCGAATCCAGCTCCGCGCGCGGGAAACGGTGATTTGGAACGGGATTTCCC	3557
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Oy	3738	GTGACGATACCTTCCATTACTAATCCATPAACATGGCTTTTGCCAACTATCTTATG	3797
Db	4407	GTGACGATACCTTCCATTACTAATCCATPAACATGGCTTTTGCCAACTATCTTATG	4348
Oy	3798	GCTAATAGCCAACTACTCTGCTCTTACAGACCTGACACGACCTCTGATATTTTACAGATG	3857
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Oy	3858	GGGTCCCATTTATTTTAAACAATCAATATACAAACGCGGCTCCCGTGCCGAG	3917
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Qy	4038	CTCATGCTGCGTCCGGCAGCTCCTTGGTCTTAAAGTGTAGGCGCAGCTTAGGCGACACAC	4097				
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Qy	4218	AGAAATGTCAGGCGAGCTGATGTTGTTGTTATTTCTGATTAAGATGACAGGTAATCTCCGTTGC	4277				
Db	3927	AGAAATGTCAGGCGAGCTGATGTTGTTGTTATTTCTGATTAAGATGACAGGTAATCTCCGTTGC	3868				
Qy	4278	GGTGCTGTTAACGGGAGGCGCAGTGTAGTCTGAGCAGTACTCGTTGTCGCGCGCGC	4337				
Db	3867	GGTGCTGTTAACGGTGGAGGCGCAGTGTAGTCTGAGCAGTACTCGTTGTCGCGCGCGC	3808				
Qy	4338	CACGAGCATATATAGCTGACAGACTTAAAGACTGCTTCTTCATGGGCTCTTTCTGCGAG	4397				
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VERSION	AX776820.1	GI:32694262					
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ORGANISM	unidentified						
REFERENCE	1	unclassified.					
AUTHORS	Haynes, J. R. and Arrington, J. E.						
TITLE	Nucleic acid adjuvants						
JOURNAL	Patent: WO 03004055-A 2 16-JAN-2003;						
	Powderject Vaccines, Inc. (US)						
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LOCUS AX776823 5089 bp DNA linear PAT 14-JUL-2003

DEFINITION Sequence 5 from Patent WO03004055.

ACCESSION AX776823

VERSION AX776823.1 GI:32694265

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

ORIGIN

Query Match

Best Local Similarity

Matches 2598; Conservative 0; Mismatches 197; Indels 41; Gaps 6;

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DEFINITION Sequence 6 from Patent WO03004055.
ACCESSION AX776824
VERSION AX776824.1 GI:32694266
KEYWORDS
SOURCE unidentifed
ORGANISM unidentifed
REFERENCE 1
AUTHORS Haynes,J.R. and Arrington,J.E.
TITLE Nucleic acid adjuvants
JOURNAL Patent: WO 03004055-A 6 16-JAN-2003;
Powderject Vaccines, Inc. (US)
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location/Qualifiers
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ORIGIN

Query Match 37.1%; Score 2378.8; DB 6; Length 5488;
Best local Similarity 91.6%; Pred. No. 0;
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VERSION AX776822.1 GI:32694264
KEYWORDS
SOURCE unidentifed
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AUTHORS Haynes, J.R. and Arrington, J.E.
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            Unpublished
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Query March 31.5%; Score 20.0.8; DB 12; Length 9918; Best Local Similarity 87.5%; Pred. No. 0; Matches 2409; Conservative 0; Mismatches 17; Indels 328; Gaps 5;									
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RESULT 12

AX138933 5108 bp DNA linear PAT 30-MAY-2001

DEFINITION Sequence 52 from Patent EP1052286.
AX138933
VERSION AX138933.1 GI:14274638KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE

1
AUTHORS Morsey, M.A. and Shepard, M.G.
TITLE Growth hormone and growth hormone releasing hormone compositions
JOURNAL Patent: EP 1052286-A 52 15-NOV-2000;
Pfizer Products Inc. (US)
FEATURES
source location/Qualifiers
1. 5108

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RESULT 13
BD000697 5108 bp DNA linear PAT 31-JAN-2002
LOCUS BD000697
DEFINITION Growth hormone and growth hormone-releasing hormone composition.
ACCESSION BD000697

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Db 3256 AATATGACATTTATATGCTCATATGTCAAATATGACCGCAATGTAATGATTTATG 3315
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RESULT 14
BD000698 5108 bp DNA linear PAT 31-JAN-2002
LOCUS Growth hormone and growth hormone-releasing hormone composition.
ACCESSION BD000698.1 GI:18623811
VERSION JP 2000350590-A/51.
KEYWORDS JP 2000350590-A/51.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 5108)
AUTHORS Morsey,M.A. and George,M.
TITLE Growth hormone and growth hormone-releasing hormone composition
JOURNAL Patent: JP 2000350590-A 51 19-DEC-2000;
PRIZER PROD INC

COMMENT
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PN JP 2000350590-A/51
PD 19-DEC-2000
PR 12-APR-2000 JP 2000111120
PI MOHAMED ALI MORSEY MICHAEL GEORGE
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ORIGIN
Query Match 31.3%; Score 2008.6; DB 6; Length 5108;
Best Local Similarity 74.2%; Pred. No. 0;
Matches 3058; Conservative 0; Mismatches 239; Indels 826; Gaps 8;

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DB 1802 CGTCCGCTCAAGTCAAGCTAATGCTGCGAGTGTAAACCAATTAACCAATTCGATT 1861
QY 587 AGAAAACTCATTGACATCAAAATGAATGCAATTTATTCATATCAGATTATCAATAC 646
DB 1862 AGAAAACTCATTGACATCAAAATGAATGCAATTTATTCATATCAGATTATCAATAC 1921
QY 647 CATTTTGTGAAAAACCGTTTCTGTAATGAAGAGAGAAAACTCAGGAGGAGTTCATTA 706
DB 1922 CATTTTGTGAAAAACCGTTTCTGTAATGAAGAGAGAAAACTCAGGAGGAGTTCATTA 1981
QY 707 GGATGGCAAGATCTGATCGGTCTGCGATTCCGATCGTCCAAATCAATCAACTTA 766
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DB 2162 CATTAAGCTGATCAATAATCACTGCAATCAACCAAAACCGTATTCATTGATGATTCG 2221
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DB 2282 GCAACCGCGCGCAGAAACCTGCCAGCGCATCAACAAATTTTCACTGCAATCGATATT 2341
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DB 2462 GTCGACCATCTCATCTGTAACATCAATGCGCAAGCTACTTTCGCAATGTTTCAAAACA 2521
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DB 2522 ACTCTGCGCATGCGGCTTCCCATCAATGATGATGATGCGACCGATTTGCGCGCAT 2581
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 QY 1607 CCTGCATAGCCTCAGGTTACTCATATPACTTTAGATTGATTTAAATCTCATTTTAA 1666
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 Db 2885 GCACATT----- 2891
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DEFINITION Sequence 55 from Patent EP1052286.
ACCESSION AX138936
VERSION AX138936.1 GI:14274641
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Morsey, M.A. and Sheppard, M.G.
TITLE Growth hormone and growth hormone releasing hormone compositions
JOURNAL Patent: EP 1052286-A 55 15-NOV-2000;
Pfizer Products Inc. (US)
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Best Local Similarity 74.2%; Pred. No. 0;
Matches 3058; Conservative 0; Mismatches 239; Indels 826; Gaps 8;

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Db	2642	TCGAGCAAGAGAGTTCCTCGTTGAATATGSCATAAACCCCTTGTAATCTGTTTATGT	2701
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Db	2702	AAGCAGACAGTTTATTTGTTTCATGATGATATATTTTATCTTGCAATGPAACATAGA	2761
OY	1487	GATTTTGGAGACAAAGTGGCTTTTCCCGCCCCCTGACAGCGTTTCTCTTTTCCCA	1546
Db	2762	GATTTTGGAGACAAAGTGGCTTTTCCCGCCCCCTGACAGCGTTTCTCTTTTCCCA	2797
OY	1547	CCCCACCCCCCAAGTTGGGGTGAAGGCCACAGGCTCGACCCAAGTCGGGGCGGACGC	1606
Db	2798	-----	2797
OY	1607	CCTGCATAGCCTCAGGTTACTCATATATCTTTAGATTGATTTTAAATCTCATTTTAA	1666
Db	2798	-----ATTATTTAGAGCATTTTATCAGGGTTATTTGCT	2828
OY	1667	TTTAAAGATCTAGTGAAGATCCTTTTGATATATCATGACCAAAATCCCTTAAAGT	1726
Db	2829	CATGACGGATATACATATTTGAATGATTTAGAAAA--ATAAACAATAGGGGTTCCGC	2884
OY	1727	GAGTTTTCGTTCCACTAGCGTCAGACCCCGTAGAAAAAGATCAAAAGATCTTCTTGAGAT	1786
Db	2885	GCACATTT-----	2891
OY	1787	CCTTTTTTCTGCGGTATATCGTCTGTGCAAACAAAACCAACCGCTACAGCGGTG	1846
Db	2892	-----TCCCGAAAGTGGCACCTGACGTTAAGAAACCATTTATATCA-----	2935
OY	1847	GTTTGTTTGGCGATCAAGAGCTACCAACTTTTTCCGAAGTAACTGCGCTTCAGCAGA	1906
Db	2936	-----	2935
OY	1907	GCGCAGATACCAATATCTGTTCTTCTAGTAGACCGTAGTTAGGCCACCACTTCAAGAAC	1966
Db	2936	-----	2935
OY	1967	TCTGTAGCACCGCCTTACATACCTCGCTGCTAATCCGTTACAGTGGCTGCGCAGT	2026
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OY	2027	GCGCATAGCTGTGCTTTACCGGGTTGACTCAAGACGATGTTTACCGGATAGAGCGCAG	2086
Db	2970	GCCCTTGTGCTT-----	2982
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OY	2147	GAACTGAATACCTTACAGCTGTAGCTATGAGAAAAGCGCACGCTTCCCGAAGGAGAAG	2206
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OY	2207	GCGCAGAGTATCCCGGTAGCGGACGGGTTCGGAAACAGAGAGACGCAACAGAGGAGCTTCCA	2266
Db	3037	GGTACACAGCTTGTCTGTAGACGG-ATGCCGGAGAGACAAAGCCCGTACAGGGCGCGCTACG	3095
OY	2267	GGGGGAAACGCTGATCTTTATATGTCCTGTGGGTTTGCACACTTGAATTGAGCGT	2326
Db	3096	CGGG-----	3099
OY	2327	CGATTTTGTGTGCTCGTCAAGGGGGGCGAGCCTATGAAAAAACGCCAGCAACGGGAC	2386
Db	3100	-----	3099
OY	2387	TTTTTACGTTCCCTGGCCTTTTGTCTGGCCTTTTGCTCACATGTTCTTCCGCGTTATCC	2446
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OY	2447	CCTGATTCGTGATTAACCGGATTAACCGCCATGCAATGATTAATATGATCAATTAAC	2506

Db	3100	-----	3099
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Oy	3227	ACCATGTGATACGGGTTTTGGCAGTACACCAATGGGGGTGGATATGCGTTTGAATCTCACGG	3286
Db	3676	ACCATGTGATACGGGTTTTGGCAGTACATCATATGGGGGTGGATATGCGTTTGAATCTCACGG	3735
Oy	3287	GGAATTTCCAAGTCTCCACCCCATTTGACGTCAATGGAGATTTGTTTGGACCAAAATCAAA	3346
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QY 4007 CATCCGAGCCCTGCTCCCATGCTCCGAGCGGCTCATGCTGCTGGGAGCTCTTGTCTCC 4066
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Job time : 24056 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2004, 14:01:32 ; Search time 14701 Seconds
(without alignments)
13016.568 Million cell updates/sec

Title: US-09-996-128A-1

Perfect score: 6408

Sequence: 1 atctctgacgatccacccacac.....tctattttaaaacccgga 6408

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*
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2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
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11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1180.4	18.4	1932	11	AK014619 Mus muscu
2	885.8	13.8	1063	12	BM463960 AGENCOURT
3	874.6	13.6	984	13	BU190117 AGENCOURT
4	849.4	13.3	1068	12	BM557397 AGENCOURT

5	837	13.1	903	13	BU183039
6	829.4	12.9	866	13 <td>BO682227</td>	BO682227
7	828.4	12.9	943	13 <td>BO677071</td>	BO677071
8	817.4	12.8	926	13 <td>BO424642</td>	BO424642
9	793.4	12.4	908	13 <td>BO424713</td>	BO424713
10	791.8	12.4	902	12 <td>BG575202</td>	BG575202
11	787.6	12.3	965	12 <td>BG576440</td>	BG576440
12	786.6	12.3	1004	9 <td>AJ281480</td>	AJ281480
13	779.4	12.2	800	9 <td>AJ281449</td>	AJ281449
14	772.2	12.1	939	13 <td>BU179860</td>	BU179860
15	762	11.9	940	13 <td>BU191334</td>	BU191334
16	760.2	11.9	766	12 <td>BG765715</td>	BG765715
17	758.6	11.8	1070	9 <td>AJ281552</td>	AJ281552
18	756	11.8	764	12 <td>BI859609</td>	BI859609
19	749.4	11.7	751	12 <td>BG574431</td>	BG574431
20	747	11.7	844	28 <td>BZ574513</td>	BZ574513
21	741.6	11.6	842	13 <td>BU189475</td>	BU189475
22	736.8	11.5	898	13 <td>BU154819</td>	BU154819
23	726.8	11.3	872	13 <td>BO424558</td>	BO424558
24	726.2	11.3	939	12 <td>BG764646</td>	BG764646
25	721.2	11.3	1574	28 <td>BZ572566</td>	BZ572566
26	704.8	11.0	988	29 <td>CNS06X6V</td>	CNS06X6V
27	704.8	11.0	889	14 <td>CF577494</td>	CF577494
28	700.8	10.9	1073	14 <td>CF269652</td>	CF269652
29	700	10.9	700	13 <td>BO660293</td>	BO660293
30	699.6	10.9	950	12 <td>BM453335</td>	BM453335
31	699	10.9	700	14 <td>CA305674</td>	CA305674
32	694	10.8	811	29 <td>ATH517156</td>	ATH517156
33	692.8	10.8	907	13 <td>BO683341</td>	BO683341
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35	689.6	10.8	859	28 <td>BZ574002</td>	BZ574002
36	687	10.7	1340	28 <td>BZ572620</td>	BZ572620
37	685.6	10.7	896	28 <td>BZ577395</td>	BZ577395
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39	682.4	10.6	733	28 <td>BZ048997</td>	BZ048997
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42	679	10.6	691	14 <td>CB864071</td>	CB864071
43	677.4	10.5	1208	28 <td>BZ577775</td>	BZ577775
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ALIGNMENTS

RESULT 1
AK014619
LOCUS
DEFINITION
Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4633402C07 product:tyrosinase, full insert sequence.
ACCESSION
AK014619
VERSION
AK014619.1 GI:12852585
KEYWORDS
HTC, CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. Normalization and subtractions of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL
MEDLINE
PUBMED
REFERENCE
3

AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P., Komio, H., Akiyama, J., Nishii, K., Kizumaki, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaiguchi, S., Ikegami, T., Kashiwagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsubiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuzaki, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
JOURNAL	RIKEN integrated sequence analysis (RISA) system--384-format
MEDLINE	sequencing pipeline with 384 multicapillary sequencer
PUBMED	Genome Res. 10 (11), 1757-1771 (2000)
REFERENCE	20530913
AUTHORS	11076861
TITLE	4
JOURNAL	The RIKEN Genome Exploration Research Group Phase II Team and the
MEDLINE	FANTOM Consortium.
PUBMED	Functional annotation of a full-length mouse cDNA collection
REFERENCE	Nature 409, 685-690 (2001)
AUTHORS	5
TITLE	The FANTOM Consortium and the RIKEN Genome Exploration Research
JOURNAL	Group Phase I & II Team.
MEDLINE	Analysis of the mouse transcriptome based on functional annotation
PUBMED	of 60,770 full-length cDNAs
REFERENCE	Nature 420, 563-573 (2002)
AUTHORS	6 (bases 1 to 1932)
TITLE	Adachi, T., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
JOURNAL	Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,
MEDLINE	Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,
PUBMED	Hishioaka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,
REFERENCE	Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Komio, H., Kouda, M.,
AUTHORS	Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,
JOURNAL	Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,
MEDLINE	Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
PUBMED	Shibata, K., Shibata, Y., Shingagawa, A., Shiraki, T., Sogabe, Y.,
REFERENCE	Shibasaki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,
AUTHORS	Tejima, Y., Toyota, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
JOURNAL	Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
MEDLINE	Direct Submission
PUBMED	Submitted (10-UTR-2000) Yoshinohide Hayashizaki. The Institute of
REFERENCE	Physical and Chemical Research (RIKEN), Laboratory for Genome
AUTHORS	Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
JOURNAL	RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
MEDLINE	Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,
PUBMED	url: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
REFERENCE	Fax: 81-45-503-9216)
AUTHORS	Please visit our web site (http://genome.gsc.riken.go.jp/) for
JOURNAL	further details.
MEDLINE	cDNA library was prepared and sequenced in Mouse Genome
PUBMED	Encyclopedia Project of Genome Exploration Research Group in Riken
REFERENCE	Genomic Sciences Center and Genome Science Laboratory in RIKEN.
AUTHORS	Division of Experimental Animal Research in Riken contributed to
JOURNAL	prepare mouse tissues. First strand cDNA was primed with a primer
MEDLINE	[5'-GAGAGAGAGATTCGAGTAAATTAATTAATTAATTCACCCCGCCCGCC 3']. cDNA was
PUBMED	prepared by using retrocote thermo-activated reverse transcriptase
REFERENCE	and subsequently enriched for full-length by cap-trapper. cDNA went
AUTHORS	through one round of normalization to Rct = 10.0 and subtraction to
JOURNAL	Rct = 100.0. Second strand cDNA was prepared with the primer
MEDLINE	adapter of sequence [5'
PUBMED	GAGAGAGAGATTCGAGTAAATTAATTAATTAATTAATTCACCCCGCCCGCC 3']. cDNA was
REFERENCE	cloned into pGEMT vector. cDNA was sequenced with BamHI and XhoI. cDNA of size comprised longer than 7 kb was
AUTHORS	selected before cloning. Vector: a modified phage-script KS(+) after
JOURNAL	bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI, 3'
MEDLINE	end: BamHI. Host: DH10B.
PUBMED	Location/Qualifiers
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REFERENCE	/db_xref="MG1:1903271"
AUTHORS	/db_xref="taxon:10090"
JOURNAL	/clone="4633402C07"
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PUBMED	/clone_lib="RIKEN full-length enriched mouse cDNA library"

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ORIGIN

Query Match 18.4%; Score 1180.4; DB 11; Length 1932;
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Matches 1375; Conservative 0; Mismatches 271; Indels 12; Gaps 2;

Oy 4509 GGGAAGAATGCTCGTCGTGCTGTTTGTNACTGCCTGCTGTGAATTCCAGACTTCGGCTGG 4568
Db 95 GGAGAATAATGTTCTTGCTGTTTGTATATGCTCTGTGAGTTTCAGATCTCTGATGG 154
Oy 4569 CCATTTCCCTTAGAGCCTGTGTCTCTTAAGAACCTATGAGAAAGAAATGCTGCCACC 4628
Db 155 CCATTTTCCTGACACCTGTGCCTCTCTTAAGAACTTGTGGCAAAGAAATGCTGCCACC 214
Oy 4629 GTGAGAGCGGGGACAGAGTCCCTGTGGCCAGACTTTCAGGACAGAGTTCCTGTCAATAT 4688
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Oy 4689 CTTTCTGTCCAMTGCACCACTTGGGCTCAATTTCCCTTCAACAGGGTGAATGACCGGAA 4748
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Oy 4869 GGTGAGAGAAACATCTTCGATTTGAGTGGCCCCAGAGAAAGACAATTTTTTGTCTACT 4928
Db 455 GATTAGAAAGAAACATTTTATTTGATGTGTCTCCGAAAAGATTAAGTCTTTTCTTACT 514
Oy 4929 CACTTTAGCAAGCATTCATCAGCTCAGACTATGTATCCCATAGGAACCTATGGCCA 4988
Db 515 CACTTTAGCAAAACATCTATCAAGCTCAGCTATGTATCTCCCAACAGGACCTATATGGCCA 574
Oy 4989 AATGAAAAATGATCAACCCCATGTTTAAACGATCAATATTTATAGACCTCTTGTCTG 5048
Db 575 AATGAAACAATGGTCAACCCCATGTTTAAATGATATAACTATCAACACTCTTGTATG 634
Oy 5049 GATGCAATTAATATGTGCAATGATGATGATGCTTTGGGGATATGAAATCTGAGAGACAT 5108
Db 635 GATGCAATTAATATGTGCAAGGACACACTGCTTTGGGGGCTCTGAATATAGAGAGACAT 694
Oy 5109 TGATTTTCCCATGAGACCAAGCTTTTGTGCTTGGCATAGACTCTTCTTGTGGCGGT 5168
Db 695 TGATTTTCCCATGAGACCAAGGCTTTGTGCTTGGCATAGACTCTTCTTGTATGTGT 754
Oy 5169 GGAACAAGAAATCCAGAAGCTGACAGGATGAAACTTCACTATTCCATATTGGGACTG 5228

Db	755	GGAA	CAGAAATTCGAGAACTTA	ACTACGGGGATGAGAACTTCA	CTGTCCATCTCGGAAATG	814													
Qy	5229	GGGGATG	CAGAAAAGTGTG	CAATTTGCA	CAGATGATGATCA	TGGGAGGTCA	GACACCCAC	5288											
Db	815	GAGAGATG	CAAAAACTGTGA	CATTGAC	AGATGA	TGAGTACTTTGGGAGGTCT	CGTCA	874											
Qy	5289	AAATCTTA	CTTA	CT	CAGCCGAGCAT	TA	CTTCCCTTGGGAGATTTG	CTGAGCG	5348										
Db	875	AAATCTTA	CTTA	CT	CAGCCGAGCAT	TA	CTTCCCTTGGGAGATTTG	CTGAGCG	934										
Qy	5349	ATTGGAG	AGTACAA	CAGCCCAT	CTAGTCTTTAT	TGCAATGAA	CGCCGAGGGAC	CTTTACG	5408										
Db	935	ATCGA	AGATATATAT	TAGCCAT	TGAGTTTAT	TGGATG	TGAA	CACTGAGGACCATAT	994										
Qy	5409	GCGTAT	CTTG	GAACCA	TCATGACAA	TCCAGAA	CCCCAAGGCT	CCCCCTT	CACTGATGT	5468									
Db	995	ACGTAT	CTTG	GAACCA	TCATGACAA	TCCAGAA	CCCCAAGGCT	CCCCCTT	CACTGATGT	1054									
Qy	5469	AGAA	TTTTG	CCGTA	GGTTG	ACCCCA	TATGAA	CTGTGCT	CCAT	TGCA	TAAAGCG	CCCAAT	5528						
Db	1055	GGAATTT	GTCTG	AGTTTG	ACCCAGTA	GAAT	TGGAT	TCAT	TGATG	TA	GA	CTG	CCCAAT	1114					
Qy	5529	CAGCTTT	GAAATAC	ACTCTG	GAAGATTT	TGCTAGT	CACTTA	CTG	GGATAG	CGAT	CGCTC	5588							
Db	1115	CAGCTTT	GAAATAC	ACTCTG	GAAGATTT	TGCTAGT	CACTTA	CTG	GGATAG	CGAT	CGCTC	1174							
Qy	5589	TCMAAG	CAGATG	CA	CAATGCTT	GCACAT	CTATAT	TGAT	GA	TG	GA	TG	CA	5648					
Db	1175	TCMAAG	CAGATG	CA	CAATGCTT	GCACAT	CTATAT	TGAT	GA	TG	GA	TG	CA	1234					
Qy	5649	GGGAT	CTG	GCACAG	TCTAT	CTTCT	CTTCA	CCAT	TCAT	TCAT	TCAT	TCAT	TCAT	5708					
Db	1235	GGGAT	CTG	GCACAG	TCTAT	CTTCT	CTTCA	CCAT	TCAT	TCAT	TCAT	TCAT	TCAT	1294					
Qy	5709	GCA	TG	GGCTCC	GAA	GCA	CCGCT	CTCTT	CA	GA	AGTTTAT	CCAG	AGCCAT	5768					
Db	1295	ACAAT	GGCTG	GAA	GCA	CCGCT	CTCTT	CA	GA	AGTTTAT	CCAG	AGCCAT	5768						
Qy	5769	TGGA	CA	TATAC	CCGGGA	TCTTA	CAT	GTGCT	CTTTA	TAC	CA	CTGTA	CAGAA	TG	GTGAT	5828			
Db	1355	CGGC	CA	TATAC	CCGGGA	TCTTA	CAT	GTGCT	CTTTA	TAC	CA	CTGTA	CAGAA	TG	GTGAT	1414			
Qy	5829	CTTAT	TTT	CAT	CCAAGAT	CTG	GGGTAT	GAT	CTAT	TG	CA	GAAT	TC	CA	CCCA	5888			
Db	1415	CTTAT	TTT	CAT	CCAAGAT	CTG	GGGTAT	GAT	CTAT	TG	CA	GAAT	TC	CA	CCCA	1474			
Qy	5889	CTCTTT	CA	AGCTA	CTA	TTA	AGTCC	TAT	TGGA	CA	CA	AGGTCC	GA	CT	GTG	TCAT	5948		
Db	1475	CTTTA	CA	AGCTA	CTA	TTA	AGTCC	TAT	TGGA	CA	CA	AGGTCC	GA	CT	GTG	TCAT	1534		
Qy	5949	CTT	TG	GGGCG	GATG	TG	TG	GGGCG	CGT	CTCT	CA	CTG	CCCTG	CT	G	CA	GGGCT	6008	
Db	1535	CTT	TG	GGGCG	GATG	TG	TG	GGGCG	CGT	CTCT	CA	CTG	CCCTG	CT	G	CA	GGGCT	6008	
Qy	6009	GCTGT	GTG	GTG	CTC	-----	-ACA	AGA	AGAG	CGCT	CTG	TGA	AAAAAG	CA	GGCA	CT	CT	6058	
Db	1555	GCTAT	GC	CTTCA	GA	GA	GA	GA	GA	GA	GA	GA	GA	GA	GA	GA	GA	1658	
Qy	6060	CATG	AGAA	AGAG	ATTAC	CA	CAGCT	---	TGT	AT	CA	GA	GC	CA	CTTAT	TA	AA	GGCT	6118
Db	1655	CATG	AGAA	AGAG	ATTAC	CA	CAGCT	---	TGT	AT	CA	GA	GC	CA	CTTAT	TA	AA	GGCT	6118
Qy	6117	AAT	AT	AGT	TG	GGG	CA	AAAA	AG	CT	GA	CT	TC	CA	CT	TA	CT	6154	
Db	1715	AACA	GAT	GGG	CA	AAAA	AG	CT	GA	CT	TC	CA	CT	TA	CT	TA	CT	1752	

RESULT 2					
BM463960					
LOCUS					
DEFINITION	BM463960	1063 bp	mRNA	linear	EST 05-FEB-2001
ACCESSION	AGENCOURT 6445513	NIH_MGC_72	Homo sapiens	cDNA clone IMAGE:5539977	
	5', mRNA sequence.				
	BM463960				

VERSION	KEYWORDS	EST.	BM463960.1	GI:18513002
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/ .			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgsab@emall.nih.gov Tissue Procurement: ATCC/DCTP/DMP			
	CDNA Library Preparation: Life Technologies, Inc.			
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)			
	DNA Sequencing by: Agencourt Bioscience Corporation			
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:			
	http://image.lnl.gov			
	Plate: LLM1235	row: 5	column: 10	
	High quality sequence stop: 749.			
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	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/clone="IMAGE:5539977"			
	/tissue_type="melanotic melanoma"			
	/lab_host="DH10B (phage-resistant)"			
	/clone_lib="NIH MGC 72"			
	/note="Organ: skin; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2 kb. Library constructed by Life Technologies."			
ORIGIN				
Query Match	13.8%;	Score 885.8;	DB 12;	Length 1063;
Best Local Similarity	96.1%;	Pred. No. 3e-243;		
Matches 937;	Conservative 0;	Matches 33;	Indels 5;	Gaps 3;
4497	TGGTGAATTC	CGGGAAGAATGCTCCGGCGCTTTTGACTGCGTGGAGATTCCA		4556
94	TGTGAGACTAGAGAGAAGATGCTTCGGCGCTTTGTACTGCGCTGTGGAATTCCA			153
4557	GACCTCGCGTGGCATTTCCTTAGAGCCTGTGTCTCTCTAAGAAGCTGATGAGAGA			4618
154	GACCTCGCGTGGCATTTCCTTAGAGCCTGTGTCTCTCTAAGAAGCTGATGAGAGA			213
4617	ATGCTGTCCACCGTGGAGCGGGGACAGGAGTCCCTGTGGCCAGCTTTACGACGAGTTT			4678
214	ATGCTGTCCACCGTGGAGCGGGGACAGGAGTCCCTGTGGCCAGCTTTACGACGAGTTT			273
4677	CTGTCAGAATATCTTCTGTCCATGACCACTTGGGCTCAATTTCCCTTACAGGGGT			4738
274	CTGTCAGAATATCTTCTGTCCATGACCACTTGGGCTCAATTTCCCTTACAGGGGT			333
4737	GGATGACCGGGAGTGTGGGCTTCCGCTTTTATATAGACTGCGAGTCTCTGGAA			4798
334	GGATGACCGGGAGTGTGGGCTTCCGCTTTTATATAGACTGCGAGTCTCTGGAA			393
4797	CTTCAATGGGATTCACCTGTGGAACTGCAAGTTTGGCTTTTGGGACCAACTGACAGA			4856
394	CTTCAATGGGATTCACCTGTGGAACTGCAAGTTTGGCTTTTGGGACCAACTGACAGA			453
4857	GAGACGACTCTTGGTGAAGAACAATTTGATTAGTGGCCCAAGAGAGCAATTT			4916
454	GAGACGACTCTTGGTGAAGAACAATTTGATTAGTGGCCCAAGAGAGCAATTT			513
4917	TTTTGGCTACCTCACTTTAGCAAGACATACATGAGCTCAGACTATGCAATCCCATAGG			4976
514	TTTTGGCTACCTCACTTTAGCAAGACATACATGAGCTCAGACTATGCAATCCCATAGG			573
4977	GACCTATGGCCAAATGAAAAATGATCAACCAATGTTTAAACGACATCAATATTATGA			5036

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Db 574 GACCTATGGCCAATGAAAATGGATCAACACCATGTTAAACACATCAATATTTATGA 633
|||
Qy 5037 CCTCTTTGTGTGATGATATATATGTGTCAATGATGACCTGTTGGGGATATGAAAT 5096
|||
Db 634 CCTCTTTGTGTGATGATATATATGTGTCAATGATGACCTGTTGGGGATATGAAAT 693
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Qy 5097 CTGAGAGACATGATTTTCCCATGAGCAGCCGCTTTCTGCTTGGCATGACTCTT 5156
|||
Db 694 CTGAGAGACATGATTTTCCCATGAGCAGCCGCTTTCTGCTTGGCATGACTCTT 753
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Qy 5157 CTTGTTGCGGTGGAGACAAGAAATCCAGAACTGACAGAGATGAAAATTTCACTATTC 5216
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Db 754 CTTGTTGCGGTGGAGACAAGAAATCCAGAACTGACAGAGATGAAAATTTCACTATTC 813
|||
Qy 5217 ATATTTGGAGCTGGCGGGATGCAAGAAAGTGAATTTGACAGATGATGATGAGGAGG 5276
|||
Db 814 ATATTTGAGCTGGCGGGATGCAAGAAAGTGAATTTGACAGATGATGATGAGGAGG 873
|||
Qy 5277 TCAGCAGCCCAACAATCTTAATCTCAAGCCAGCATCTTCTCTCTTGGCAGAT 5336
|||
Db 874 TCAGCAGCCCAACAATCTTAATCTCAAGCCAGCATCTTCTCTCTTGGCAGAT 932
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Qy 5337 TGTCTGTAGCCGATGAGAGATGACAAAGCCATCACTTTTATGCAATGAAAGCCCGA 5396
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Db 933 TGTCTGTAGCCGATGAGAGATGACAAAGCCATCACTTTTATGCAATGAAAGCCCGA 992
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Qy 5397 GGAACCTTTACGGGTATCTCTGGAACCATGACAAATCCAGAACCCCAAGGCTCCCTC 5456
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Db 993 GGAACCTTTACGGGTATCTCTGGAACCATGACAAATCCAGAACCCCAAGGCTCCCTC 1048
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Qy 5457 TTCAGCTGATGAGA 5471
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Db 1049 TTCAGCTGATGAGA 1063
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RESULT 3
BU190117 984 bp mRNA linear EST 04-SEP-2002
LOCUS BU190117
DEFINITION Agencourt_8076683 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6089012
5', mRNA sequence.
ACCESSION BU190117
VERSION BU190117.1 GI:22704101
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 984)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
[found through the I.M.A.G.E. Consortium/LNL at:](http://image.lnl.gov)
<http://image.lnl.gov>
Plate: LNCM328 row: b column: 21
High quality sequence: 661.
Location/Qualifiers

FEATURES
Source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6089012"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_112"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:

EcORI: cDNA made by oligo-dT priming. Directionally cloned
into EcORI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Subscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 13 6%; Score 874.6; DB 13; Length 984;
Best Local Similarity 96.6%; Pred. No. 4,8e-240;
Matches 926; Conservative 0; Mismatches 29; Indels 4; Gaps 3;

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Qy 4570 CATTTCCCTAGAGCTGTGTCTCTCTTAAGAACTGTATGAGAGAAATGCTGCCAG 4629
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Db 64 CATTTCCCTAGAGCTGTGTCTCTCTTAAGAACTGTATGAGAGAAATGCTGCCAG 123
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Qy 4630 TGAAGGGGAGACAGAGTCCCTGTGSCAGCTTTTCAAGAGAGTCCCTGTAGATATC 4689
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Qy 4690 CTTCTGTCCAAATGACACCACTTGGGCTCAATTTCCCTTCAAGAGGCTGATGACCGGAG 4749
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Db 184 CTTCTGTCCAAATGACACCACTTGGGCTCAATTTCCCTTCAAGAGGCTGATGACCGGAG 243
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Qy 4750 TGTGTGCTTCCGCTCTTTTATATAGAGCTGTGCACTGCTCTGGAACAATTGATTC 4809
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Db 244 TGTGTGCTTCCGCTCTTTTATATAGAGCTGTGCACTGCTGTGGAACAATTGATTC 303
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Qy 4810 AACTGTGAGAACTGCAAGTTTGGCTTTTGGGGACCAACTGCAAGAGAGACGACTCTTG 4869
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Db 304 AACTGTGAGAACTGCAAGTTTGGCTTTTGGGGACCAACTGCAAGAGAGACGACTCTTG 363
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Db 364 GTGAGAGAAACATCTTTCGATTTGAGTGGCCCGCAGAGAGACAAATTTTGGCTACTC 423
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Qy 4930 ACTTTAGCAAGATACATCACTGCTGACATGTATGATCCCATAGAGACTATGGCCAA 4989
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Db 424 ACTTTAGCAAGATACATCACTGCTGACATGTATGATCCCATAGAGACTATGGCCAA 483
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Qy 4990 ATGAAAAATGAGATCAACCCATGTTTAAGCATCAATATTATGACCTTTGTCTGG 5049
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Db 484 ATGAAAAATGAGATCAACCCATGTTTAAGCATCAATATTATGACCTTTGTCTGG 543
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Qy 5050 ATGCATTTATATGTGTCAATGATGACATGCTTGGGGATATGAAATCTGAGAGACATT 5109
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Db 544 ATGCATTTATATGTGTCAATGATGACATGCTTGGGGATATGAAATCTGAGAGACATT 603
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Qy 5110 GATTTTGGCCATGAGACACAGCTTTTGTGCTTGGCATGACTCTTCTTGTGGGTGG 5169
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Db 604 GATTTTGGCCATGAGACACAGCTTTTGTGCTTGGCATGACTCTTCTTGTGGGTGG 663
|||
Qy 5170 GAACAAAGAAATCCAGAACTGACAGAGATGAAAAATTCACTATTTCCATTTGGGACTGG 5229
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Db 664 GAACAAAGAAATCCAGAACTGACAGAGATGAAAAATTCACTATTTCCATTTGGGACTGG 723
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Qy 5230 CGGATGACAGAAAGTGTGATTTTGCATGATGATGATGATGATGATGATGATGATGATG 5289
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Qy 5290 AATCTTAATCTTACTGAGCCGAGCATCTTCTCTCTTGTGAGATGCTGTAGCCGA 5349
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Db 784 AATCTTAATCTTACTGAGCCGAGCATCTTCTCTCTTGTGAGATGCTGTAGCCGA 843
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Qy 5350 -TTGAGAGATGACAAAGCATGATCTTATGCAATGG--AACGCCAGAGGAGCTTTA 5406
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Db 844 TTGAGAGATGACAAAGCATGATCTTATGCAATGGAAAGCCGAGGAGGAGCTTTA 903
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Dy 5407 CGCG-TAATCTGAAACCATGCATAATCCAGAACCCCAAGCCTCCCCCTTTCAGCTG 5468

Dd 904 CGCGTTAATCTGAAACCATGCACAATCCGAAAACCCCAAGGGCTCCCCCTTTCAG 962

RESULT 4

LOCUS	BMS57397	1068 bp	mRNA	linear	EST 20-FEB-2002
DEFINITION	AGENCOURT_6561703 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5547850				
	5', mRNA sequence.				

FEATURES

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/mol_type="mRNA"
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/clone="IMAGE:5547850"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NH_MGC-72"
/note="Organ: Skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. primer: Oligo dT
Average insert size 2 kb. Library constructed by Life
Technologies."

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Query Match	13.3%;	Score 849.4;	DB 12;	Length 1068;
Best Local Similarity	93.9%;	Pred. No. 9.6e-233;		

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Db	405	GAGACGACTCTTGTTGAGGAAGAAACATCTTCGATTGTGAATGTCGCCCAAGAAAGGACAAATT	464
Qy	4917	TTTTGGCTTACCTCACTTTAGCAAGCAATACATCAGCTCAGACTAGTGCATGCCCATAGG	4976
Db	465	TTTTGGCTTACCTCACTTTAGCAAGCAATACATCAGCTCAGACTAGTGCATGCCCATAGG	524
Qy	4977	GACCTATGGCCAAATGAAAAATGGATCAACACCATGTTTAAACGACATCAATATTTATGA	5036
Db	525	GACCTATGGCCAAATGAAAAATGGATCAACACCATGTTTAAACGACATCAATATTTATGA	584
Qy	5037	CCTCTTTGTCGATGCAATTAATTAATGTGTCAATGATGCACTGCTTGGGGGATATGAAAT	5096
Db	585	CCCTCTTTGTCGATGCAATTAATTAATGTGTCAATGATGCACTGCTTGGGGGATATGAAAT	644
Qy	5097	CTGAGAGCAATTGATTTTGGCCCATGGAAGCAACAGCTTTCTGCTTGGCATGACATCTT	5156
Db	645	CTGAGAGCAATTGATTTTGGCCCATGGAAGCAACAGCTTTCTGCTTGGCATGACATCTT	704
Qy	5157	CTTGTTCGCGTGGGAACAAGAAATCCAGAAGCTGACAGAGATGAAAACTTCACTATTC	5216
Db	705	CTTGTTCGCGTGGGAACAAGAAATCCAGAAGCTGACAGAGATGAAAACTTCACTATTC	764
Qy	5217	ATATT--GGGACTGGCGGGATGCAAGAAAAGTGTGCAATTTGCAACAGATGAGTACAT--GGGA	5274
Db	765	ATATTGGGGAATGGCGGGATGCAAGAAAAGTGTGCAATTTGCAACAGATGAGTACAT--GGGA	824
Qy	5275	GGTACGACACCCCA--CAAAATCCCTAACTTAATCAGCCCAATCATTTCTTCTCTTGGCA	5333
Db	825	GGTACGACACCCCA--CAAAATCCCTAACTTAATCAGCCCAATCATTTCTTCTCTTGGCA	884
Qy	5334	GATTGTCTGATCCGA--TTGGAGAGATCAACAAGCCATCAGTC--TTTATGCAATGGAAGC	5391
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Db	1005	CCCCTCTTCAGCTGATGTAATAATTTTGTGCTGATTTTGAACCAATATGAAATCGGGTT	1064
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Db	1065	C 1065	

RESULT 5

[illegible]

479/ CTTCAATGGGATTCAACTGTGGAACTGCACAGTTTGGCTTTTGGGGACCAACTGCACAGA 485

cdNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation

4629 GTGGAGGGGAGAGAGTCCCTGTGGCAGCTTTCAAGGAGAGTTCTGTGAGATAT 4688
122 GTGGAGGGGAGAGAGTCCCTGTGGCAGCTTTCAAGGAGAGTTCTGTGAGATAT 181
4689 CCTTCTGTCCAAATGACCACTTGGGCTCAATTTCCCTTCAAGGGGTGATGCCGGA 4748
182 CCTTCTGTCCAAATGACCACTTGGGCTCAATTTCCCTTCAAGGGGTGATGCCGGA 241
4749 GTCTGTGCTTCCCTTTTATATATAGAGCTGCCAGTCTCTGGCAATTCATGGAT 4808
242 GTCTGTGCTTCCCTTTTATATATAGAGCTGCCAGTCTCTGGCAATTCATGGAT 301
4809 CAATGTGGAAACGTGCAAGTTGGCTTTGGGGACCAACGTGCAAGAGAGAGCACTT 4868
302 CAATGTGGAAACGTGCAAGTTGGCTTTGGGGACCAACGTGCAAGAGAGAGCACTT 361
4869 GGTGAGAGAAACATCTTCCATTTGAGTGGCCCCAGAGAGAGCAAAATTTTGGCTTACT 4928
362 GGTGAGAGAAACATCTTCCATTTGAGTGGCCCCAGAGAGAGCAAAATTTTGGCTTACT 421
4929 CACTTGAAGAAAGCATACCATCAGCTCAGCTATGTCATCCCATAGGAGACTATGGCA 4988
422 CACTTGAAGAAAGCATACCATCAGCTCAGCTATGTCATCCCATAGGAGACTATGGCA 481
4989 AATGAAAAATGATCAACACCCATGTTAAGCATCATATTTATAGACCTCTTGTCTG 5048
482 AATGAAAAATGATCAACACCCATGTTAAGCATCATATTTATAGACCTCTTGTCTG 541
5049 GATCATTTATATGTGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 5108
542 GATCATTTATATGTGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 601
5109 TGATTTTGGCCATGAGACAGCAGCTTTCTGCTTGGCATGATCTTCTTGTGGCTG 5168
602 TGATTTTGGCCATGAGACAGCAGCTTTCTGCTTGGCATGATCTTCTTGTGGCTG 661
5169 GGAACAAGAAATCCAGAAAGTGTGACATTTGACAGATGATGATGATGATGATGATGAT 5228
662 GGAACAAGAAATCCAGAAAGTGTGACATTTGACAGATGATGATGATGATGATGATGAT 721
5229 GCGGATGACAGAAAGTGTGACATTTGACAGATGATGATGATGATGATGATGATGATGAT 5288
722 GCGGATGACAGAAAGTGTGACATTTGACAGATGATGATGATGATGATGATGATGATGAT 781
5289 AATCTTAATCTTACTGAGCCAGCATCTTCTCTCTTGGAGATGATGATGATGATGATGAT 5347
782 AATCTTAATCTTACTGAGCCAGCATCTTCTCTCTTGGAGATGATGATGATGATGATGAT 841
5348 GATTGAGAGATCAACAGCC 5368
842 GATTGAGAGATCAACAGCC 862

RESULT 7
LOCUS B0677071 943 bp mRNA linear EST 15-JUL-2002
DEFINITION AGENCOURT 8209637 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6272720
5', mRNA sequence.
ACCESSION B0677071
VERSION B0677071.1 GI:21789750
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 943)
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: scapbs-remail.nih.gov
Tissue Procurement: DCTD/DBP

CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LCM2451 row: 1 column: 09
High quality sequence stop: 636.
Location/Qualifiers
Source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6272720"
/issue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOT87; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 12.9%; Score 828.4; DB 13; Length 943;
Best Local Similarity 97.7%; Pred. No. 1e-26;
Matches 881; Conservative 0; Mismatches 15; Indels 6; Gaps 4;
5089 TATGAATTCGAGAGACATATTTTGGCCATGAAAGCACCCTTTCTGCTTGGCAT 5148
1 TCGAAATCTGAGAGAG-ATGATTTTGGCCATGAAAGCACCCTTTCTGCTTGGCAT 59
5149 AGACTCTTCTTGTGGGCTGAGAGAAAGATCCAGAGCTGACAGAGATGAAATCTTC 5208
60 AGACTCTTCTTGTGGGCTGAGAGAAAGATCCAGAGCTGACAGAGATGAAATCTTC 119
5209 ACTATTCATATTTGGAGCTGGCGGATGCAAGAAAGTGTGACATTTGACAGATGAT 5268
120 ACTATTCATATTTGGAGCTGGCGGATGCAAGAAAGTGTGACATTTGACAGATGAT 179
5269 ATGGAGATGATGACACCCCAATCTTAATCTGACGCCAGCATCTTCTCTCTCT 5328
180 ATGGAGATGATGACACCCCAATCTTAATCTGACGCCAGCATCTTCTCTCTCTCT 239
5329 TGGCAGATTTGCTGTAGCCGATTTGAGAGATCAACAGCCATGATCTTATGCAATGGA 5388
240 TGGCAGATTTGCTGTAGCCGATTTGAGAGATCAACAGCCATGATCTTATGCAATGGA 299
5389 ACGCCGAGGAGACCTTTACGCGCTAATCTGGAACCATGACAAATCCAGAACCCCAAG 5448
300 ACGCCGAGGAGACCTTTAAGCGCTAATCTGGAACCATGACAAATCCAGAACCCCAAG 359
5449 CTCCCTCTTCACTGATGATGATTTTGGCTTGAAGTTGACCCAAATGATCTGGTCC 5508
360 CTCCCTCTTCACTGATGATGATTTTGGCTTGAAGTTGACCCAAATGATCTGGTCC 419
5509 ATGGATTAAGCTGCAATTTCACTTGAAGATTAACATGGAAGATTTGCTAGCCACT 5568
420 ATGGATTAAGCTGCAATTTCACTTGAAGATTAACATGGAAGATTTGCTAGCCACT 479
5569 ACTGGATAGCGGATGCTTCAAGAGAGATGACATGCTTGGACATCTATATGAAT 5628
480 ACTGGATAGCGGATGCTTCAAGAGAGATGACATGCTTGGACATCTATATGAAT 539
5629 GGAACAATGTCCAGGTACAGGATCTGCCAAGATCTTATCTTCTTCCATGCA 5688
540 GGAACAATGTCCAGGTACAGGATCTGCCAAGATCTTATCTTCTTCCATGCA 599
5689 TTGTGACAGATTTTGTGAGCAGTGGCTCCGAAGGACCGTCTCTCAAGAGATTAT 5748

Db 600 TTGTGTGACAGTATTTTGTGACAGTGGCTCCAAAGGACCGTCTCTTCAAGAAGTTTAT 659
QY 5749 CCAGAGGCCAATGACCACTTGGACATTAACCGGGAAATCTTACATGGTTCTTTTATACCA 5808
Db 660 CCAGAGGCCAATGACCACTTGGACATTAACCGGGAAATCTTACATGGTTCTTTTATACCA 719
QY 5809 CTGTACAGAAATGGTGTATTTCTTTATTTTCATCCAAAGATGGGCTATGACTATAGCTAT 5868
Db 720 CTGTACAGAAATGGTGTATTTCTTTATTTTCAT-CAAGATCTGGGCTATGACTATAGCTAT 778
QY 5869 CTACAGATTCAGAACCCAGACTCTTTTCAAGACTTACCTTAAGTCTTAATTTGAACAAG-C 5927
Db 779 CTACAGATTCAGAACCCAGACTCTTTTCAAGACTTACCTTAAGTCTTAATTTGAACAAGCC 838
QY 5928 GAGTCGGATCTGGTCTATGCTCTTGGGGGCGGCGA---TGATAGGGGCGGCTCTCACTGC 5984
Db 839 GAGTCGGATCTGGTCTATGCTCTTGGGGGCGGCGAATAAGAAAGGGGCTCTCTCACTGC 898
QY 5985 CC 5986
Db 899 CC 900

RESULT 8
BQ424642 926 bp mRNA linear EST 23-MAY-2002
LOCUS AGENCOURT_7926673 NIH_MGC_72 Homo sapiens cdna clone IMAGE:6160409
DEFINITION 5', mRNA sequence.
ACCESSION BQ424642
VERSION BQ424642.1 GI:21119957
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@rs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DRP
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM13511 row: a column: 18
High quality sequence stop: 628.
Location/Qualifiers

FEATURES
source 1..926
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6160409"
/issue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_11b="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6, Site_1: NotI,
Site_2: SalI; Cloned unidirectionally. Primer: 1.1go dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 12.8%; Score 817.4; DB 13; Length 926;
Best Local Similarity 96.5%; Pired. No. 1.5e-223;
Matches 888; Conservative 0; Mismatches 24; Indels 8; Gaps 5;

QY 4863 ACTCTGTGTAAGAAACATCTTCCATTTGAGTGGCCCGACAGAAAGCAATTTTTCG 4922
Db 9 ACTCTGTGTAAGAAACATCTTCCATTTGAGTGGCCCGACAGAAAGCAATTTTTCG 67

QY 4923 CTACCTCACTTTAGCAAAAGCATACATCACTGATGATGATATCCCATAGGACCTA 4982
Db 68 CTACCTCACTTTAGCAAAAGCATACATCACTGATGATGATATCCCATAGGACCTA 127
QY 4983 TGGCCAAATGAAAATATGATCAACACCTGTTTAAACGATCAATATTTATGACTCTT 5042
Db 128 TGGCCAAATGAAAATATGATCAACACCTGTTTAAACGATCAATATTTATGACTCTT 187
QY 5043 TGTCTGATGATATATATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5102
Db 188 TGTCTGATGATATATATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 247
QY 5103 AGACATTTGATTTTGGCCATGAAGCAACACCTTTTCTGCTTGGCATATGATCTTTTGT 5162
Db 248 AGACATTTGATTTTGGCCATGAAGCAACACCTTTTCTGCTTGGCATATGATCTTTTGT 307
QY 5163 GCGGTGGGAACAAGAAATCCAGAGCTGACAGAGATGAAAACCTTCACTTTCATTTG 5222
Db 308 GCGGTGGGAACAAGAAATCCAGAGCTGACAGAGATGAAAACCTTCACTTTCATTTG 367
QY 5223 GGAATGGCGGATGACAGAAAAGTGTGACATTTTGACAGATGATGATGATGATGATGATGAT 5282
Db 368 GGAATGGCGGATGACAGAAAAGTGTGACATTTTGACAGATGATGATGATGATGATGATGAT 427
QY 5283 CCCCAAAATCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTA 5342
Db 428 CCCCAAAATCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTA 487
QY 5343 TAGCCATTTGGAGAGTATCAACAGCCATCATGCTTTTATGATGAAAGCCCGAGGAGC 5402
Db 488 TAGCCATTTGGAGAGTATCAACAGCCATCATGCTTTTATGATGAAAGCCCGAGGAGC 547
QY 5403 TTTAGGGGCTTAATCCGGAACCATGACAAATCCAGAACCCCAAGGCTCCCTCTTACG 5462
Db 548 TTTAGGGGCTTAATCCGGAACCATGACAAATCCAGAACCCCAAGGCTCCCTCTTACG 607
QY 5463 TGAATGAAATTTTGGCTGATTTGACCCCAATATGAAATGATGATGATGATGATGATGAT 5522
Db 608 TGAATGAAATTTTGGCTGATTTGAC--TTGACCAATATGAAATGATGATGATGATGATGAT 666
QY 5523 CAATTTCACTTTAAGAAATACACTGGAAGATTTTGTATCTTCACTTGGATAGCGGA 5582
Db 667 CAATTTCACTTTAAGAAATACACTGGAAGATTTTGTATCTTCACTTGGATAGCGGA 726
QY 5583 TGCCCTCAAGAGAGATGACAAATGCTTGGACATCTTATGAAATGAAACATAT-CCC 5641
Db 727 TGCCCTCAAGAGAGATGACAAATGCTTGGACATCTTATGAAATGAAACATATGTCGCC 786
QY 5642 AGGTACAGGAGATCTGCAACAGATCTTATCTTCTTTCACCATGATTTGTG--ACA 5698
Db 787 AGGTACAGGAGATCTGCAACAGATCTTATCTTCTTTCACCATGATTTGTGCAAGT 846
QY 5699 GATATTTTGAAGATGCTGCTCCGAGGACCGTCC--TCTTCAAGAGTTTATTCAGAAC 5756
Db 847 AATTTTGAAGATGCTGCTCCGAGGACCGTCC--TCTTCAAGAGTTTATTCAGAAC 906
QY 5757 CAATGACCCCATTTGACATTA 5776
Db 907 CAATGACCCCATTTGACATTA 926

RESULT 9
BQ424713 908 bp mRNA linear EST 23-MAY-2002
LOCUS AGENCOURT_7926435 NIH_MGC_72 Homo sapiens cdna clone IMAGE:6160418
DEFINITION 5', mRNA sequence.
ACCESSION BQ424713
VERSION BQ424713.1 GI:21120028
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

QY 4557 GACCTCCGCTGGCATTTCCTTAGAGCCTGTGTCTCTTAAGAACTGATGGAAGGA 4616
 DB 96 GACCTCCGCTGGCATTTCCTTAGAGCCTGTGTCTCTTAAGAACTGATGGAAGGA 155
 QY 4617 ATCTGTCCACCGTGAGCGGGGACAGAGTCCCTGTGGCAGCTTTCAGGAGAGTTC 4676
 DB 156 ATCTGTCCACCGTGAGCGGGGACAGAGTCCCTGTGGCAGCTTTCAGGAGAGTTC 215
 QY 4677 CTGTCAAGATATCTCTTGTGCAATGACCACTTGGGCTCAATTTCCCTTCA 4736
 DB 216 CTGTCAAGATATCTCTTGTGCAATGACCACTTGGGCTCAATTTCCCTTCA 275
 QY 4737 GGAATGACCGGGAGTCCGTGCTTCTTTTAAATAGGACTGCGACAGTCTTGCCA 4796
 DB 276 GGAATGACCGGGAGTCCGTGCTTCTTTTAAATAGGACTGCGACAGTCTTGCCA 335
 QY 4797 CTTCATGGAGTTCACCTGTGGAATCTGCAAGTTTGGCTTTGGGACCAATGCAAGA 4856
 DB 336 CTTCATGGAGTTCACCTGTGGAATCTGCAAGTTTGGCTTTGGGACCAATGCAAGA 395
 QY 4857 GAGACGACTCTTGGTGAGAAAGAAATCTTGCATTTGAGTCCCGCAGAGAGCAAAAT 4916
 DB 396 GAGACGACTCTTGGTGAGAAAGAAATCTTGCATTTGAGTCCCGCAGAGAGCAAAAT 455
 QY 4917 TTTTGGCTACTCACTTACCAAGCAATACCTAGCTGAGCTATGTCAATCCCATAGG 4976
 DB 456 TTTTGGCTACTCACTTACCAAGCAATACCTAGCTGAGCTATGTCAATCCCATAGG 515
 QY 4977 GACCTATGGCAATGAAAAATGGAATCAACACCATGTTTAAAGCAATCAATTTTATGA 5036
 DB 516 GACCTATGGCAATGAAAAATGGAATCAACACCATGTTTAAAGCAATCAATTTTATGA 575
 QY 5037 CCTCTTTGTCTGATGATTTATATGTGCAATGATGACCTGCTGGGGATATGAAT 5096
 DB 576 CCTCTTTGTCTGATGATTTATATGTGCAATGATGACCTGCTGGGGATATGAAT 635
 QY 5097 CTGAGAGATGATTTTGGCCATGAGACCAAGCTTTTCTGCTTGGATGACTCTT 5156
 DB 636 CTGAGAGATGATTTTGGCCATGAGACCAAGCTTTTCTGCTTGGATGACTCTT 695
 QY 5157 CTGTTGGCGTGGGAAACAAGAAATCCAGAACTGACAGAGATGAAGAAAC-TTCACTATTC 5215
 DB 696 CTGTTGGCGTGGGAAACAAGAAATCCAGAACTGACAGAGATGAAGAAAC-TTCACTATTC 755
 QY 5216 CATATTTGGGACTGCGGGATGACAGAAAGTGTGACATTTGCACAGATGATAGATC-GGGA 5274
 DB 756 CATATTTGGGACTGCGGGATGACAGAAAGTGTGACATTTGCACAGATGATAGATC-GGGA 815
 QY 5275 GGTGACGACCCCAAAATCTTAATTAAGTCAAGCCAGATCAATTTCTCTTGGCAG 5334
 DB 816 GGTGACGACCCCAAAATCTTAATTAAGTCAAGCCAGATCAATTTCTCTTGGCAG 875
 QY 5335 ATTGTCTGTACCGGATTTGAGAGATAC 5361
 DB 876 AATTGTCTGTACCGGATTTGAGAGATAC 902
 RESULT 11
 LOCUS BG576440 965 bp mRNA linear EST 10-APR-2001
 DEFINITION 602555683F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4708629 5',
 mRNA sequence.
 ACCESSION BG576440
 VERSION BG576440.1 GI:13584093
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 965)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: DCTD/DTF
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 plate: LLNL0580 row: 5 column: 22
 High quality sequence sfop: 737.
 Location/Qualifiers
 1..965
 source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4708629"
 /rname_type="mammary adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: breast; Vector: pCMV-Sport6; Site: 1: NotI;
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.383 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 12.3%; Score 787.6; DB 12; Length 965;
 Best Local Similarity 94.1%; Pred. No. 6.3e-215;
 Matches 886; Conservative 0; Mismatches 44; Indels 12; Gaps 6;

QY 5228 GCGGGATGCAAGAAAGTGTGACATTTGACAGATGATGAGAGTCAAGACCCCA 5287
 DB 23 GCGGGATGCAAGAAAGTGTGACATTTGACAGATGATGAGAGTCAAGACCCCA 82
 QY 5288 CAATCTTAATCTTACACCCAGATCAATTTCTCTCTTGGAGATTTGCTGAGCC 5347
 DB 83 CAATCTTAATCTTACACCCAGATCAATTTCTCTCTTGGAGATTTGCTGAGCC 142
 QY 5348 GATTGAGAGATGACAAACAGCCATCACTTATGCAATGAGAAAGCCGAGGACCTTAC 5407
 DB 143 GATTGAGAGATGACAAACAGCCATCACTTATGCAATGAGAAAGCCGAGGACCTTAC 202
 QY 5408 GGGGTATCTGGAACCAATGACAAATCCAGAACCCCAAGGCTCCCTTTCAGCTGATG 5467
 DB 203 GGGGTATCTGGAACCAATGACAAATCCAGAACCCCAAGGCTCCCTTTCAGCTGATG 262
 QY 5468 TAGAATTTTGGCTGAGTTGACCCATATGATCTGTGCTCATGATTAAGCTGCCAAT 5527
 DB 263 TAGAATTTTGGCTGAGTTGACCCATATGATCTGTGCTCATGATTAAGCTGCCAAT 322
 QY 5528 TCAGCTTTGAATACACTGAGAGATTTGCTAGTCACTTACTGGGATGAGGATGCT 5587
 DB 323 TCAGCTTTGAATACACTGAGAGATTTGCTAGTCACTTACTGGGATGAGGATGCT 382
 QY 5588 CTCAAAGCAGATGACAAATGCTTGCACATCTATATGATGAGAAACAATGTCACAGTAC 5647
 DB 383 CTCAAAGCAGATGACAAATGCTTGCACATCTATATGATGAGAAACAATGTCACAGTAC 442
 QY 5648 AGGATCTGCCAAGCATCTTATCTTCTTTCACACGATTTTGTGACATATTTTGG 5707
 DB 443 AGGATCTGCCAAGCATCTTATCTTCTTTCACACGATTTTGTGACATATTTTGG 502
 QY 5708 AGCAGTGGCTCGAAGGACCGTCTCTCAAGAGTTTATCCAGAGCCATGACCA 5767
 DB 503 AGCAGTGGCTCGAAGGACCGTCTCTCAAGAGTTTATCCAGAGCCATGACCA 562
 QY 5768 TTGACATTAACCGGAGATCTAATGTTCTTTTATACACTGTACAGAAATGTTGA-T 5826
 DB 563 TTGACATTAACCGGAGATCTAATGTTCTTTTATACACTGTACAGAAATGTTGA-T 622
 QY 5827 TTCTTATTTCAATCCAAAGATCTGGGCTATGACTATAGTATCTACAGATTCAGACCA 5886

Db 623 TTCTTATTTCATCCAAAGATCTGGGCTATGACTATATGCTATCTCAAGATTACAGCCCA 682

QY 5887 GACTCTTTCAAGACTCATTAAGTCTATTGGAAACAAGAGTCCGATCTGGTCATGG 5946

Db 683 GACTCTTTCAAGACTCATTAAGTCTATTGGAAACAAGAGTCCGATCTGGTCATGG 742

QY 5947 CTCCTTGGGCGCGG-ATGGTATGGGGCGCTCTCACTGCCCTGCTGGCAGGGCTTGGAG 6005

Db 743 CTCCTTGGAGCGGGCAAGGTAGGGGCGCTCTCACTGCCCTGCTGGCAGGGCTTGGAG 802

QY 6006 CTGCTGTGTCTGTCAAGAGAA---AGCAGCTTCTGTGAAGAAACAGCCTCTC---C 6058

Db 803 CTGCTGTGTCTGTCAAGAGAAACAGCCTTGTGAAGAAACAGCCTCTCTC 862

QY 6059 TCATGAGAAAGAGATTACACAGCTTGATC-AGAGCATTATATAAGGCTTA--GG 6115

Db 863 ATGGCGGAAGAAAGATACCAACAGCTTGATCAAGAGCCATATATACACGCGCTAAGGC 922

QY 6116 CAATGAGTAGGGGCAAAAAGCCTGACCTCACTCACTCA 6157

Db 923 AATTGAGGTAGGCAAAAAGCCTGACTAATCTCA 964

RESULT 12
AJ281480/c 1004 bp mRNA linear EST 30-JUN-2000

LOCUS 4A3A-P4G8-F Anopheles gambiae immune competent 4A3A Anopheles

DEFINITION gambiae CDNA clone 4A3A-P4G8, mRNA sequence.

ACCESSION AJ281480

VERSION AJ281480.1 GI:6929360

KEYWORDS EST.

SOURCE Anopheles gambiae (African malaria mosquito)

ORGANISM Anopheles gambiae
Eukaryote; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.

REFERENCE 1 (bases 1 to 1004)
Dimopoulos, G., Casavant, T.L., Chang, S., Scheetz, T., Roberts, C., Donohue, M., Schultz, J., Benez, V., Bork, P., Ansoorge, W., Soares, M.B. and Kafatos, F.C.
Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)

JOURNAL MEDLINE 20300950

PUBMED 10841561

COMMENT Contact: Dimopoulos G
Fotis C. Kafatos laboratory
European Molecular Biology Laboratory
Meyhofstrasse 1, 69117 Heidelberg, Germany.
Location/Qualifiers
1. 1004

FEATURES
Source
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="4A r/r"
/db_xref="taxon:7165"
/clone="4A3A-P4G8"
/cell_line="immune competent 4A3A"
/lab_host="E. coli DH10B"
/note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; sequenced from forward priming site which reads from the 3' end of the cDNA. The 4A3A is a directionally cloned and normalized cDNA library that was constructed from the 4A3A cell line oligo-T primed cDNA according to: Bonaldo, Lennon & Soares (1996) : Normalization and Subtraction: Two approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."

ORIGIN
Query Match 12.3%; Score 786.6; DB 9; Length 1004;
Best Local Similarity 99.4%; Pred. No. 1.3e-214;
Matches 789; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1615 AGCCTCAGGTATCTCATATATATCTTATAGATTATTAATTAATTTAAAG 1674

Db 794 AGACCAAGTTTACTCATATATATCTTATAGATTATTAATTAATTTAAAG 725

QY 1675 GATCTAGGTGAAGATCTTTTATATCTATGACCAAAATCCCTTAACGTATTC 1734

Db 734 GATCTAGGTGAAGATCTTTTATATCTATGACCAAAATCCCTTAACGTATTC 675

QY 1735 GTTCCACTAGAGGTGACGCCGTAGAAAAGATCAAGAGATCTTCTAGATCTTTT 1794

Db 674 GTTCCACTAGAGGTGACGCCGTAGAAAAGATCAAGAGATCTTCTAGATCTTTT 615

QY 1795 TCTGCCGTATATCTGCTGCTTGAACAAAAACACAGCCTACAGCGGTGTTGTT 1854

Db 614 TCTGCCGTATATCTGCTGCTTGAACAAAAACACAGCCTACAGCGGTGTTGTT 555

QY 1855 GCCGATCAAGAGCTACCACTCTTTTCCGAAAGTATCTGCTTCAAGAGCGAGAT 1914

Db 554 GCCGATCAAGAGCTACCACTCTTTTCCGAAAGTATCTGCTTCAAGAGCGAGAT 495

QY 1915 ACCAATATCTGTTCTTCTATGATGAGCCGTATGAGCCACCACTTCAAGAACTGTAGC 1974

Db 494 ACCAATATCTGTTCTTCTATGATGAGCCGTATGAGCCACCACTTCAAGAACTGTAGC 435

QY 1975 ACCGCTACATACCTGCTGCTTGAARCCGTATACAGAGTGGCTGCGAGGAGATA 2034

Db 434 ACCGCTACATACCTGCTGCTTGAARCCGTATACAGAGTGGCTGCGAGGAGATA 375

QY 2035 GTGCTGCTTACCGGGTTGACTCAAGAGCATAGTTACCGGATAGGCGGAGCGTGGG 2094

Db 374 GTGCTGCTTACCGGGTTGACTCAAGAGCATAGTTACCGGATAGGCGGAGCGTGGG 315

QY 2095 CTGAACGGGGGGTTCGTGCAACAGCCAGCTTGAGCGAAGCACTACCGAATCTGAG 2154

Db 314 CTGAACGGGGGGTTCGTGCAACAGCCAGCTTGAGCGAAGCACTACCGAATCTGAG 255

QY 2155 ATACCTACAGCGGAGCTATGAGAAAGCGCAGCTTCCGAAAGGGAGAAAGCGGACAG 2214

Db 254 ATACCTACAGCGGAGCTATGAGAAAGCGCAGCTTCCGAAAGGGAGAAAGCGGACAG 195

QY 2215 GTATCCGTAAAGCGGAGCGGATCGGAACAGGAGAGCCACAGAGGAGCTTCCAGGGGAAA 2274

Db 194 GTATCCGTAAAGCGGAGCGGATCGGAACAGGAGAGCCACAGAGGAGCTTCCAGGGGAAA 135

QY 2275 CGCCTGTATCTTATATAGTCTGTGCGGTTTCCACCTTGACTTGAAGCGTGATTTT 2334

Db 134 CGCCTGTATCTTATATAGTCTGTGCGGTTTCCACCTTGACTTGAAGCGTGATTTT 75

QY 2335 GTATGCTGTCAAGGGGGGAGAGCTTATGAGAAAAAGCCAGCAAGCGGCTTTTACG 2394

Db 74 GTATGCTGTCAAGGGGGGAGAGCTTATGAGAAAAAGCCAGCAAGCGGCTTTTACG 15

QY 2395 GTTCTGGGCTTTT 2408

Db 14 GTTCTGGGCTTTT 1

RESULT 13
AJ281449/c 800 bp mRNA linear EST 30-JUN-2000

LOCUS 4A3A-P4D5-F Anopheles gambiae immune competent 4A3A Anopheles

DEFINITION gambiae CDNA clone 4A3A-P4D5, mRNA sequence.

ACCESSION AJ281449

VERSION AJ281449.1 GI:6929329

KEYWORDS EST.

SOURCE Anopheles gambiae (African malaria mosquito)

ORGANISM Anopheles gambiae
Eukaryote; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.

REFERENCE 1 (bases 1 to 800)
Dimopoulos, G., Casavant, T.L., Chang, S., Scheetz, T., Roberts, C.,

Donohue, M., Schultz, V., Benes, V., Bork, P., Ansoorge, W., Soares, M.B. and Kafatos, F.C.
 Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines
 Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)

JOURNAL MEDLINE PUBMED
 10841561
 20300950

COMMENT
 Contact: Dimopoulos G
 Fotis C. Kafatos Laboratory
 European Molecular Biology Laboratory
 Meyerhofstrasse 1, 69117 Heidelberg, Germany.
 Location/Qualifiers
 1. 800
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="4a r/r"
 /db_xref="taxon:7165"
 /clone="4A3A-P4D5"
 /cell_line="immune competent 4A3A"
 /lab_host="E. coli DH10B"
 /clone_lib="Anopheles gambiae immune competent 4A3A"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: EcoRI; Site 2: NotI; sequenced from forward priming site which reads from the 3' end of the cDNA. The 4A3A is a directionally cloned and normalized cDNA library that was constructed from the 4A3A cell line oligo-T primed cDNA according to: Bonaldi, Lennon & Soares (1996) : Normalization and Subtraction: Two approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."

ORIGIN

Query Match 12.2%; Score 779.4; DB 9; Length 800;
 Best Local Similarity 99.2%; Pred. No. 1.3e-212;
 Matches 783; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1636 ACTTATGATTGATTAAACCTTCAATTTTAAATTTAAAGATCTAGGTGAAGATCCTTTT 1695
 800 ACTTATGATTGATTAAACCTTCAATTTTAAATTTAAAGATCTAGGTGAAGATCCTTTT 741

1696 TGTATATTCATGACCAAAATCCCTTAACGTGATTTTCTTGCATCTGAGCGTCACAGCC 1755
 740 TGTATATTCATGACCAAAATCCCTTAACGTGATTTTCTTGCATCTGAGCGTCACAGCC 681

1756 CGTAGAAAAGATCAAGATCTTCTTGAGATCCTTTTCTGCGCGTAACTGCTGCTT 1815
 680 CGTAGAAAAGATCAAGATCTTCTTGAGATCCTTTTCTGCGCGTAACTGCTGCTT 621

1816 GCAAAACAAAAACCAACCGCTACAGCGGTGTTTGTTCGCGATCAAGAGCTACCAAC 1875
 620 GCAAAACAAAAACCAACCGCTACAGCGGTGTTTGTTCGCGATCAAGAGCTACCAAC 561

1876 TCTTTTTCGAGAGTAAGTCTGCTTACGAGAGGCGAGATCCAAATATCTGTTCTTCTAGT 1935
 560 TCTTTTTCGAGAGTAAGTCTGCTTACGAGAGGCGAGATCCAAATATCTGTTCTTCTAGT 501

1936 GTAGCGGTAGTGGCCACCACTTCAAGAACTGTGAGACCGCGCTACATACCTCGCTCT 1995
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2056 CTTAAGACATAGTTACCGGATTAAGGCGCGGCTCGGCTGAACGGGGGCTTCTGTCAC 2115
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2236 CGAAGACAGAGAGCGGACGAGAGAGAGCTTCCAGGGGAAACGCTGTATCTTATATAGTCC 2295

DB 200 CGAAGACAGAGAGCGGACGAGAGAGCTTCCAGGGGAAACGCTGTATCTTATATAGTCC 141

2296 TGTGCGGTTTCCGACCTCTGACTGAGCGTGAATTTTGTGATGCTGCTCAGGGGGGCG 2355

DB 140 TGTGCGGTTTCCGACCTCTGACTGAGCGTGAATTTTGTGATGCTGCTCAGGGGGGCG 81

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RESULT 14
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 VERSION BU179860.1 GI:22693844
 KEYWORDS EST.
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
 1 (bases 1 to 939)
 NIH-MGC http://img.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://imgc.llnl.gov
 Plate: LLCM2436 row: f column: 10
 High quality sequence stop: 606.
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 /clone="IMAGE:6266889"
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 /note="Organ: skin; Vector: pOTF7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

ORIGIN

Query Match 12.1%; Score 772.2; DB 13; Length 939;
 Best Local Similarity 93.0%; Pred. No. 1.7e-210;
 Matches 863; Conservative 0; Mismatches 56; Indels 9; Gaps 5;

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 1 AGGCTCCCTCTTACGCTATGATGAATTTTCCCTGAGTTTACCAATATGATTCGT 60


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QY      5110 GATTTTGGCCATGAGCCACGCTTTTCTGCTTGGCATAGACTCTTGTGTGGGTGG 5169
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Db      608 GATTTTGGCCATGAGCCACGCTTTTCTGCTTGGCATAGACTCTTGTGTGGGTGG 667
QY      5170 GAACAAAGAAATCCAGAGCTGACAGAGATGAAAACTTCACTATTCCATATTGGGACTGG 5229
      |||
Db      668 GAACAAAGAAATCCAGAGCTGACAGAGATGAAACTTCACTATTCCATATTGGGACTGG 727
QY      5230 CGGGATGCAAGAAAGTGTGACATTGTGACAGATGA--GTACATGGAGGTCAACCCCA 5287
Db      728 CGGGATGCAAGAAAGTGTGACATTGTGACAGATGAAGTACTTGGAGGGTCAACCA 787
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